



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 191168

TO: Juliet Switzer
Location: rem/2A61/2C70
Art Unit: 1634
Friday, June 09, 2006
Case Serial Number: 09/865579

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine.Hensle@uspto.gov

Search Notes

Examiner Switzer,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

*orange
sheet*

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 62.5679 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-18
Perfect score: 28
Sequence: 1 aaattgggtacaaagtatacttcgtt 28

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	2007	2	US-08-743-637B-169
2	28	100.0	2007	3	US-08-526-840B-169
3	28	100.0	2028	3	US-09-134-001C-1710
C 4	18.6	66.4	601	3	US-09-949-016-43987
C 5	18.6	66.4	55387	3	US-09-949-016-12993
C 6	18.4	65.7	37030	3	US-08-311-731A-25
C 7	18	64.3	232	4	US-09-880-107-262
C 8	17.8	63.6	465	3	US-09-270-767-6011
C 9	17.8	63.6	465	3	US-09-767-767-2193
10	17.6	62.9	452	3	US-08-956-171E-582
11	17.6	62.9	452	3	US-08-781-986A-582
C 12	17.6	62.9	601	3	US-09-949-016-198083
C 13	17.6	62.9	601	3	US-09-949-016-198084
C 14	17.6	62.9	792	3	US-09-583-110-2286
C 15	17.6	62.9	792	3	US-09-107-433-1010
16	17.6	62.9	4371	3	US-09-134-000C-3022
17	17.6	62.9	7263	3	US-09-562-702A-31
18	17.6	62.9	7263	3	US-09-561-818A-27
19	17.6	62.9	7263	3	US-10-037-182-19
20	17.6	62.9	7554	3	US-09-562-702A-29
21	17.6	62.9	7554	3	US-09-561-818A-25
22	17.6	62.9	7554	3	US-10-037-182-17
23	17.6	62.9	24020	3	US-09-949-016-17353

C 24 17.6 62.9 96074 3 US-09-949-016-12760
C 25 17.6 62.9 96074 3 US-09-949-016-13611
C 26 17.6 62.9 110000 3 US-09-830-902-1
C 27 17.6 62.9 4403765 3 US-09-103-840A-2
C 28 17.6 62.9 4411529 3 US-09-103-840A-1
C 29 17.4 62.1 1233 5 US-09-974-300-2472
C 30 17.4 62.1 1318 3 US-09-183-253-3
C 31 17.4 62.1 1983 3 US-09-452-638-50
C 32 17.4 62.1 1983 3 US-09-121-587A-1
C 33 17.4 62.1 3175 3 US-09-799-451-793
C 34 17.4 62.1 4249 3 US-09-071-035-403
C 35 17.4 62.1 4249 3 US-10-206-576-403
C 36 17.4 62.1 4359 3 US-09-071-035-401
C 37 17.4 62.1 4359 3 US-10-206-576-401
C 38 17.4 62.1 84495 3 US-09-797-906-3
C 39 17 60.7 220 3 US-09-513-999C-14621
C 40 17 60.7 293 3 US-09-854-133-534
C 41 17 60.7 601 3 US-09-949-016-124786
C 42 17 60.7 601 3 US-09-949-016-144670
C 43 17 60.7 601 3 US-09-949-016-144671
C 44 17 60.7 1583 4 US-10-094-743-1469
C 45 17 60.7 1761 3 US-09-248-796A-6869

ALIGNMENTS

RESULT 1

US-08-743-637B-169
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

Sequence 12760, A
Sequence 13611, A
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 2472, Ap
Sequence 3, Appli
Sequence 50, Appl
Sequence 1, Appli
Sequence 793, App
Sequence 403, App
Sequence 403, App
Sequence 401, App
Sequence 401, App
Sequence 3, Appli
Sequence 14621, A
Sequence 534, App
Sequence 124786,
Sequence 144670,
Sequence 144671,
Sequence 1469, Ap
Sequence 6869, Ap

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; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match      100.0%; Score 28; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAGATGATACCTTCGTT 28
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Db 608 AAATTGGGTACAAGATGATACCTTCGTT 635

RESULT 2
US-08-526-840B-169
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match      100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAGATGATACCTTCGTT 28
    |||||||
Db 608 AAATTGGGTACAAGATGATACCTTCGTT 635

RESULT 3
US-09-134-001C-1710
; Sequence 1710, Application US/09134001C
; Patent No. 6380370

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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12993
; LENGTH: 55387
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(55387)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-12993

Query Match      66.4%; Score 18.6; DB 3; Length 55387;
Best Local Similarity 84.0%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4 TTGGGTACAAGATGATACCTTCGTT 28
Db      20965 TTGGGTACAAGATGATACCTTCGTT 20941

RESULT 6
US-08-311-731A-25/c
; Sequence 25, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37030 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12993
; LENGTH: 55387
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(55387)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-12993

Query Match      66.4%; Score 18.6; DB 3; Length 55387;
Best Local Similarity 84.0%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4 TTGGGTACAAGATGATACCTTCGTT 28
Db      20965 TTGGGTACAAGATGATACCTTCGTT 20941

RESULT 7
US-09-880-107-262
; Sequence 262, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 262
; LENGTH: 232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 AAL29390
; US-09-880-107-262

Query Match      64.3%; Score 18; DB 4; Length 232;
Best Local Similarity 80.8%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 ATTGGGTACAAGATGATACCTTCGTT 28
Db      172 ATTGGGTACAAGATGATACCTTCGTT 197

RESULT 8
US-09-270-767-6011/c
; Sequence 6011, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6011
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-6011

Query Match      63.6%; Score 17.8; DB 3; Length 465;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ATTGGGTACAAGATGATACCT 23
Db      172 ATTGGGTACAAGATGATACCT 197
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Db      201 ATTGGGTACAGGATACCT 181

RESULT 9
US-09-270-767-21293/c
; Sequence 21293, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21293
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-21293

Query Match      63.6%; Score 17.8; DB 3; Length 465;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 ATTGGGTACAAGATGATACCT 23
Db      201 ATTGGGTACAGGATACCT 181

RESULT 10
US-08-956-171E-582
; Sequence 582, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-582
Query Match      62.9%; Score 17.6; DB 3; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAAGATGATACCTTC 25
Db      330 AATTGGTAAACAAGATAATACCTAC 353

RESULT 11
US-08-781-986A-582
; Sequence 582, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-582
Query Match      62.9%; Score 17.6; DB 3; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAAGATGATACCTTC 25
Db      330 AATTGGTAAACAAGATAATACCTAC 353

RESULT 12
US-09-949-016-198083/c
; Sequence 198083, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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; LENGTH: 452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 582:
US-08-956-171E-582

Query Match      62.9%; Score 17.6; DB 3; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAAGATGATACCTTC 25
Db      330 AATTGGTAAACAAGATAATACCTAC 353

RESULT 11
US-08-781-986A-582
; Sequence 582, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-582
Query Match      62.9%; Score 17.6; DB 3; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAAGATGATACCTTC 25
Db      330 AATTGGTAAACAAGATAATACCTAC 353

RESULT 12
US-09-949-016-198083/c
; Sequence 198083, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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Db 408 AACTTGGTCAAGCTGATAACTTC 385

RESULT 15

US-09-107-433-1010/c

; Sequence 1010, Application US/09107433

; Patent No. 6800744

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ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Denek
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1010:

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/ name: 72.2862.gp115
/
/ TYPE: nucleic acid
/
/ STRANDEDNESS: double
/
/ TOPOLOGY: circular
/
/ MOLECULE TYPE: DNA (genomic)
/
/ HYPOTHETICAL: NO
/
/ ANTI-SENSE: NO
/
/ ORIGINAL SOURCE:
/
/ ORGANISM: Streptococcus pneumoniae
/
/ FEATURE:
/
/   NAME/KEY: misc feature
/   LOCATION: (B) LOCATION 1..792
/

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; SEQUENCE DESCRIPTION: SEQ ID NO: 1010:
US-09-107-433-1010
  Query Match      62.9%; Score 17.6; DB 3; Length 792;
  Best Local Similarity 83.3%; Pred. No. 1.6e+02;
  Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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      |||||
Db      408 AACTTGGTACAGCTGATTAACCTTC 385

Search completed: May 31, 2006, 21:13:00
Job time : 66.5679 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 31, 2006, 21:16:53 ; Search time 727.424 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-18
Perfect score: 28
Sequence: 1 aaattgggtacaaatgatacttcgtt 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:
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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
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2	28	100.0	560	10 US-10-478-633A-150
3	28	100.0	1957	9 US-10-479-674-82
4	28	100.0	2007	3 US-09-452-599-169
5	28	100.0	2007	7 US-10-121-120-169
6	28	100.0	2007	9 US-10-479-674-78
7	28	100.0	2007	9 US-10-479-674-90
8	28	100.0	2007	9 US-10-121-120-169
9	28	100.0	2028	8 US-10-724-972A-3141
10	26.4	94.3	2007	9 US-10-479-674-91
11	20.6	73.6	1400	16 US-11-128-061-4115
12	20.6	73.6	1400	16 US-11-128-049-4115
13	20.6	73.6	2858	16 US-11-128-061-473
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15	20	71.4	20	10 US-10-478-633A-153
16	20	71.4	3800	8 US-10-398-221-3698
17	19.6	70.0	306	9 US-10-425-115-140327

C 18	19.6	70.0	2910	9	US-10-425-115-126781	Sequence 126781,
C 19	19.6	70.0	2931	9	US-10-425-115-126780	Sequence 126780,
C 20	19.2	68.6	595	12	US-10-301-480-472753	Sequence 472753,
C 21	19.2	68.6	595	12	US-10-301-480-1086162	Sequence 1086162,
C 22	19.2	68.6	605	4	US-09-925-065A-406025	Sequence 406025,
C 23	19.2	68.6	605	5	US-09-925-065A-406025	Sequence 406025,
C 24	19.2	68.6	576	8	US-10-282-122A-10503	Sequence 10503, A
C 25	19.2	68.6	591	8	US-10-282-122A-9815	Sequence 9815, Ap
C 26	19.2	68.6	856	12	US-10-301-480-561542	Sequence 561542,
C 27	19.2	68.6	856	12	US-10-301-480-1174951	Sequence 1174951,
C 28	19.2	68.6	879	6	US-10-027-632-8631	Sequence 8631, Ap
C 29	19.2	68.6	879	7	US-10-027-632-8631	Sequence 8631, Ap
C 30	18.6	66.4	529	7	US-10-029-386-7679	Sequence 7679, Ap
C 31	18.4	65.7	362	4	US-09-925-065A-109347	Sequence 109347,
C 32	18.4	65.7	362	5	US-09-925-065A-109347	Sequence 109347,
C 33	18.4	65.7	381	10	US-10-779-543-11069	Sequence 11069, A
C 34	18.4	65.7	381	12	US-10-301-480-465371	Sequence 465371,
C 35	18.4	65.7	381	12	US-10-301-480-1078780	Sequence 1078780,
C 36	18.4	65.7	384	4	US-09-925-065A-397844	Sequence 397844,
C 37	18.4	65.7	384	5	US-09-925-065A-397844	Sequence 397844,
C 38	18.4	65.7	395	12	US-10-301-480-210272	Sequence 210272,
C 39	18.4	65.7	395	12	US-10-301-480-823681	Sequence 823681,
C 40	18.4	65.7	396	4	US-09-925-065A-110802	Sequence 110802,
C 41	18.4	65.7	396	5	US-09-925-065A-110802	Sequence 110802,
C 42	18.4	65.7	450	4	US-09-925-065A-573590	Sequence 573590,
C 43	18.4	65.7	450	4	US-09-925-065A-573591	Sequence 573591,
C 44	18.4	65.7	450	4	US-09-925-065A-573593	Sequence 573593,
C 45	18.4	65.7	450	5	US-09-925-065A-573590	Sequence 573590,

ALIGNMENTS

RESULT 1

US-09-865-579A-18
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Saio, Juichi
; APPLICANT: Ishiguro, Takahiko
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; CURRENT APPLICATION NUMBER: 2001-05-29
; FILE REFERENCE: 9558-003-27
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-18

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAATGATACCTTCGTT 28

Db 1 AAATTGGGTACAAATGATACCTTCGTT 28

RESULT 2

US-10-478-633A-150
; Sequence 150, Application US/10478633A
; Publication No. US20050059000A1

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; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 150
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-150

Query Match      100.0%; Score 28; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAGATGATACCTTCGTT 28
Db 368 AAATTGGGTACAGATGATACCTTCGTT 395

RESULT 3
US-10-479-674-82
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTAN
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 28; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAGATGATACCTTCGTT 28
Db 559 AAATTGGGTACAGATGATACCTTCGTT 586

RESULT 4
US-09-452-599-169
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
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; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAGATGATACCTTCGTT 28
Db 608 AAATTGGGTACAGATGATACCTTCGTT 635

RESULT 5
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 28; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAGATGATACCTTCGTT 28
Db 608 AAATTGGGTACAGATGATACCTTCGTT 635

RESULT 6
US-10-479-674-78
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIST.
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; CURRENT FILING DATE: 1999-12-01
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; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 78

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-78

Query Match 100.0%; Score 28; DB 9; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28

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Db 608 AAATTGGGTACAAGATGATACCTTCGTT 635

RESULT 7

US-10-479-674-90

; Sequence 90, Application US/10479674

; Publication No. US20050019893A1

; GENERAL INFORMATION:

; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.

; APPLICANT: Huletsky, Ann

; APPLICANT: Rosebach, Valery

; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT

; FILE REFERENCE: TV/12287.92

; CURRENT APPLICATION NUMBER: US/10/479,674

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: CA 2,348,042

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 90

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-90

Query Match

Best Local Similarity 100.0%; Score 28; DB 9; Length 2007;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28

|||||

Db 609 AAATTGGGTACAAGATGATACCTTCGTT 636

RESULT 8

US-10-121-120-169

; Sequence 169, Application US/10121120

; Publication No. US20050042606A9

; GENERAL INFORMATION:

; APPLICANT: Bergeron, Michel G.

; APPLICANT: Ouellette, Marc

; APPLICANT: Roy, Paul H.

; TITLE OF INVENTION: Specific and Universal Probes and Amplification

; TITLE OF INVENTION: Primers

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial

; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical

; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

; FILE REFERENCE: 12287.31

; CURRENT APPLICATION NUMBER: US/10/121,120

; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: 09/452,599

; PRIOR FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: 08/304,732

; PRIOR FILING DATE: 1994-09-12

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 169

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-91

Query Match

Best Local Similarity 94.3%; Score 26.4; DB 9; Length 2007;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-121-120-169

Query Match

Best Local Similarity 100.0%; Score 28; DB 9; Length 2007;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28

|||||

Db 608 AAATTGGGTACAAGATGATACCTTCGTT 635

RESULT 9

US-10-724-972A-3141

; Sequence 3141, Application US/10724972A

; Publication No. US20040147734A1

; GENERAL INFORMATION:

; APPLICANT: Doucette-Stamm, Lynn

; APPLICANT: Bush, David

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: PATH03-16

; CURRENT APPLICATION NUMBER: US/10/724,972A

; CURRENT FILING DATE: 2003-12-01

; PRIOR APPLICATION NUMBER: 09/450,969

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: 09/134,001

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 7544

; SEQ ID NO 3141

; LENGTH: 2028

; TYPE: DNA

; ORGANISM: S.epidermidis

US-10-724-972A-3141

Query Match

Best Local Similarity 100.0%; Score 28; DB 8; Length 2028;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28

|||||

Db 630 AAATTGGGTACAAGATGATACCTTCGTT 657

RESULT 10

US-10-479-674-91

; Sequence 91, Application US/10479674

; Publication No. US20050019893A1

; GENERAL INFORMATION:

; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.

; APPLICANT: Huletsky, Ann

; APPLICANT: Rosebach, Valery

; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT

; FILE REFERENCE: TV/12287.92

; CURRENT APPLICATION NUMBER: US/10/479,674

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: CA 2,348,042

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 91

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-91

QY 1 AAATGGGTACAAGATGATACCTTCGTT 28
|||||
Db 609 AAATGGGTACAAGATGATACCTTCGTT 636

RESULT 11
US-11-128-061-4115/c
; Sequence 4115, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4115
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Cricetinae gen. sp.
US-11-128-061-4115

Query Match 73.6%; Score 20.6; DB 16; Length 1400;
Best Local Similarity 85.2%; Pred. No. 54;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAATGGGTACAAGATGATACCTTCGTT 28
|||||
Db 566 AAATGGGTACAATCTGAGACCTTCATT 540

RESULT 12
US-11-128-049-4115/c
; Sequence 4115, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4115
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Cricetinae gen. sp.
US-11-128-049-4115

Query Match 73.6%; Score 20.6; DB 16; Length 1400;
Best Local Similarity 85.2%; Pred. No. 54;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AATTTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 566 AATTTGGGTACAATCTGAGACCTTCATT 540

RESULT 13
US-11-128-061-473/c
; Sequence 473, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 473
; LENGTH: 2858
; TYPE: DNA
; ORGANISM: Cricetinae gen. sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (129)..(191)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (366)..(400)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (405)..(423)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (481)..(501)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1020)..(1034)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-473

Query Match 73.6%; Score 20.6; DB 16; Length 2858;
Best Local Similarity 85.2%; Pred. No. 64;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AATTTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 2024 AATTTGGGTACAATCTGAGACCTTCATT 1998

RESULT 14
US-11-128-049-473/c
; Sequence 473, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.

APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
TITLE OF INVENTION: MAKING AND USING SAME
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 473
LENGTH: 2858
TYPE: DNA
ORGANISM: Cricetinae gen. sp.
FEATURE:
NAME/KEY: misc feature
LOCATION: (129)..(191)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (366)..(400)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (405)..(423)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (481)..(501)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1020)..(1034)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-473

Query Match 73.6%; Score 20.6; DB 16; Length 2858;
Best Local Similarity 85.2%; Pred.No. 64;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AATTGGGTACAGATGATACCTTCGTT 28
|||||
Db 2024 AATTGGGTACAAATCTGAGACCTTCATT 1998

RESULT 15
US-10-478-633A-153/c
Sequence 153, Application US/10478633A
Publication No. US20050059000A1
GENERAL INFORMATION:
APPLICANT: TAKARA BIO INC.
TITLE OF INVENTION: A stabilization method and a preservation method for a reagent fo
TITLE OF INVENTION: acid amplification or detection reaction
FILE REFERENCE: 663232
CURRENT APPLICATION NUMBER: US/10/478,633A
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: JP 2001-177737
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: JP 2001-249689
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 153
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Designed chimeric oligonucleotide primer designated as Meca-A611
OTHER INFORMATION: amplify a portion of Meca gene from Staphylococcus aureus. "Nucle
OTHER INFORMATION: are ribonucleotides-other nucleotides are deoxyribonucleotides."
US-10-478-633A-153

Query Match 71.4%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred.No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGGTACAAAGATGATACCT 23
|||||
Db 20 TTGGGTACAAAGATGATACCT 1

Search completed: May 31, 2006, 23:02:16
Job time : 728.424 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 10.716 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-18
Perfect score: 28
Sequence: 1 aaattgggtacaaatgatacttcggtt 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246937 seqs, 5886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.6	62.9	1397	6	US-10-953-349-20718
2	17	60.7	2367	7	US-11-121-154-185
3	16.8	60.0	966	7	US-11-217-529-174552
4	16.8	60.0	1476	7	US-11-217-529-304
5	16.8	60.0	3561	7	US-11-121-154-58
6	16.8	60.0	16351	6	US-10-501-834-217
7	16.4	58.6	660	6	US-10-953-349-6113
8	16.4	58.6	1852	6	US-10-953-349-14597
9	16.2	57.9	25	7	US-11-217-529-105721
10	16.2	57.9	351	7	US-11-217-529-77397
11	16.2	57.9	3054	6	US-10-505-928-492
12	16	57.1	378	7	US-11-217-529-82662
13	16	57.1	1501	6	US-10-953-349-3885
14	16	57.1	1811	6	US-10-953-349-28833
15	16	57.1	1821	6	US-10-953-349-5704
16	15.8	56.4	606	7	US-11-249-111-27
17	15.8	56.4	756	7	US-11-217-529-82078
18	15.8	56.4	1200	7	US-11-217-529-79719
19	15.8	56.4	1309	6	US-10-953-349-7709
20	15.8	56.4	1347	7	US-11-217-529-76835
21	15.8	56.4	2896	7	US-11-293-697-987
22	15.8	56.4	3165	7	US-11-217-529-75763
23	15.6	55.7	521	6	US-10-488-619-2432
24	15.6	55.7	728	6	US-10-953-349-37612
25	15.6	55.7	1566	6	US-10-953-349-8326

26	15.4	55.0	876	6	US-10-953-349-20501
27	15.4	55.0	903	7	US-11-217-529-76302
28	15.4	55.0	1038	6	US-10-953-349-3387
29	15.4	55.0	1181	6	US-10-953-349-21841
30	15.4	55.0	1293	7	US-11-217-529-82762
31	15.4	55.0	1332	6	US-10-953-349-12881
32	15.4	55.0	2250	6	US-10-953-349-7298
33	15.4	55.0	2847	7	US-11-293-697-403
34	15.4	55.0	2913	7	US-11-217-529-3195
35	15.4	55.0	3252	7	US-11-217-529-885
36	15.4	55.0	3252	7	US-11-217-529-76569
37	15.4	55.0	3339	7	US-11-217-529-5429
38	15.4	55.0	4534	6	US-10-473-691B-1
39	15.4	55.0	394191	6	US-10-506-549-3
40	15.2	54.3	417	7	US-11-217-529-1516
41	15.2	54.3	574	6	US-10-488-619-2128
42	15.2	54.3	603	6	US-10-488-619-84
43	15.2	54.3	631	6	US-10-488-619-2344
44	15.2	54.3	756	7	US-11-217-529-78743
45	15.2	54.3	813	6	US-10-953-349-16833

ALIGNMENTS

RESULT 1
US-10-953-349-20718
; Sequence 20718, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20718
; LENGTH: 1397
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20718

Query Match 62.9%; Score 17.6; DB 6; Length 1397;
Best Local Similarity 83.3%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAGATGATACCTT 24
Db 300 AAAATGGGTACAGAGGATACCTT 323

RESULT 2
US-11-121-154-185
; Sequence 185, Application US/111211154
; Publication No. US20060105914A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, LARRY EDMUND
; APPLICANT: WEINER, RONALD M.
; APPLICANT: HUTCHESON, STEVEN WAYNE
; APPLICANT: ERBORG, NATHAN A.
; APPLICANT: HOWARD, MICHAEL
; TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
; FILE REFERENCE: 108172-00121
; CURRENT APPLICATION NUMBER: US/11/121,154
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,971
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185
; LENGTH: 2367

; TYPE: DNA
; ORGANISM: Microbulbifer degradans
US-11-121-154-185

Query Match 60.7%; Score 17; DB 7; Length 2367;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 TTGGTACAAGATGATACCTTCGTT 28
Db 1584 TTGGCTACAAGATGGCTCTTCGTT 1608

RESULT 3
US-11-217-529-174552
; Sequence 174552, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174552
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174552

Query Match 60.0%; Score 16.8; DB 7; Length 966;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAGATGATACCTTCGTT 28
Db 242 AAAAGGGTACAACGCTGATACATCCGAT 269

RESULT 4
US-11-217-529-304
; Sequence 304, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 304
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-304

Query Match 60.0%; Score 16.8; DB 7; Length 1476;

Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TACAAGATGATACCTTCGTT 28
Db 161 TACAAGATGGTACCTTCGTT 180

RESULT 5
US-11-121-154-58
; Sequence 58, Application US/11211154
; Publication No. US20060105914A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, LARRY EDMUND
; APPLICANT: WEINER, RONALD M.
; APPLICANT: HUTCHESON, STEVEN WAYNE
; APPLICANT: EKBOG, NATHAN A.
; APPLICANT: HOWARD, MICHAEL
; TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
; FILE REFERENCE: 108172-00121
; CURRENT APPLICATION NUMBER: US/11/121,154
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,971
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Microbulbifer degradans
US-11-121-154-58

Query Match 60.0%; Score 16.8; DB 7; Length 3561;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAGATGATACCTTCGTT 28
Db 1101 AGATTGGTAAAGTGTCTACGTCGAT 1128

RESULT 6
US-10-501-834-217/c
; Sequence 217, Application US/10501834
; Publication No. US20060088828A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
; TITLE OF INVENTION: and Proteins
; FILE REFERENCE: 07039/386US1
; CURRENT APPLICATION NUMBER: US/10/501,834
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 16351
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-501-834-217

Query Match 60.0%; Score 16.8; DB 6; Length 16351;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAGATGATACCTTCGTT 28
Db 8069 AATTGGTTATAGTTTATACCTTCATT 8042

```
RESULT 7
US-10-953-349-6113
; Sequence 6113, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6113
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6113

Query Match      58.6%; Score 16.4; DB 6; Length 660;
Best Local Similarity 76.9%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 ATTGGGTACAAGATGATACCTTCGTT 28
DB 454 AATTGGTACTTGACGATACCTTCCTT 479

RESULT 8
US-10-953-349-14597
; Sequence 14597, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14597
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-14597

Query Match      58.6%; Score 16.4; DB 6; Length 1852;
Best Local Similarity 76.9%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 ATTGGGTACAAGATGATACCTTCGTT 28
DB 1657 ATTATCTAAAGATGATACCTTCGTT 1682

RESULT 9
US-11-217-529-105721/c
; Sequence 105721, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182

Query Match      57.9%; Score 16.2; DB 7; Length 351;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATTGGGTACAAGATGATAC 22
DB 33 AATTGGGTATAAGATGATAAC 13

RESULT 10
US-11-217-529-77397/c
; Sequence 77397, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77397
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77397

Query Match      57.9%; Score 16.2; DB 7; Length 351;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATTGGGTACAAGATGATAC 22
DB 33 AATTGGGTATAAGATGATAAC 13

RESULT 11
US-10-505-928-492
; Sequence 492, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 492
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-492

Query Match      57.9%; Score 16.2; DB 6; Length 3054;
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; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105721
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-105721
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Query Match      57.9%; Score 16.2; DB 7; Length 25;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 AATTGGGTACAAGATGATAC 22
DB 25 AATTGGGTATAAGATGATAAC 5
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RESULT 10
US-11-217-529-77397/c
; Sequence 77397, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77397
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77397
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Query Match      57.9%; Score 16.2; DB 7; Length 351;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 AATTGGGTACAAGATGATAC 22
DB 33 AATTGGGTATAAGATGATAAC 13
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RESULT 11
US-10-505-928-492
; Sequence 492, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 492
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-492
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Query Match      57.9%; Score 16.2; DB 6; Length 3054;
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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28833
; LENGTH: 1811
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-28833

Query Match      57.1%; Score 16; DB 6; Length 1811;
Best Local Similarity 79.2%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTT 24
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Db 961 AAATTGGTTACAAAATCATAGCCT 984

RESULT 15
US-10-953-349-5704
; Sequence 5704, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5704
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5704

Query Match      57.1%; Score 16; DB 6; Length 1821;
Best Local Similarity 79.2%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTT 24
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Db 1033 AACTTGGGTACACAGATCCACCTT 1056

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Job time : 11.716 secs

; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82662
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82662

Query Match      57.1%; Score 16; DB 7; Length 378;
Best Local Similarity 79.2%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TTGGGTACAAGATGATACCTTGGT 27
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Db 211 TTGGATACAGATCATACCTTGGT 234

RESULT 13
US-10-953-349-3885/c
; Sequence 3885, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3885
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3885

Query Match      57.1%; Score 16; DB 6; Length 1501;
Best Local Similarity 79.2%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ATTGGGTACAAGATGATACCTTCG 26
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Db 166 ATTCGGTAGAAGATGACTCCTTCG 143

RESULT 14
US-10-953-349-28833
; Sequence 28833, Application US/109533349
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 9	13	92.9	2068	2	US-08-608-452-1
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C 14	13	92.9	5265	3	US-09-620-412C-174
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C 26	12.4	88.6	50	3	US-10-131-827-258
C 27	12.4	88.6	50	5	US-10-131-831-258
C 28	12.4	88.6	399	3	US-09-583-110-1470
C 29	12.4	88.6	408	4	US-09-605-703B-1409
C 30	12.4	88.6	408	4	US-09-605-703B-1413
C 31	12.4	88.6	414	3	US-09-107-433-1001
C 32	12.4	88.6	489	3	US-09-270-767-7793
C 33	12.4	88.6	489	3	US-09-270-767-23075
C 34	12.4	88.6	601	3	US-09-949-016-26439
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C 40	12.4	88.6	601	3	US-09-949-016-58296
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C 46	12.4	88.6	601	3	US-09-949-016-188180
C 47	12.4	88.6	649	3	US-09-533-559-4801
C 48	12.4	88.6	676	3	US-09-533-559-5196
C 49	12.4	88.6	683	4	US-09-605-703B-1411
C 50	12.4	88.6	734	4	US-09-297-648-2528
C 51	12.4	88.6	759	5	US-09-974-300-2230
C 52	12.4	88.6	765	3	US-09-614-221A-450
C 53	12.4	88.6	807	3	US-08-961-527-357
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C 55	12.4	88.6	834	3	US-09-495-050A-288
C 56	12.4	88.6	863	10	5223425-1
C 57	12.4	88.6	863	10	5223425-9
C 58	12.4	88.6	940	3	US-09-023-655-667
C 59	12.4	88.6	1029	2	US-07-809-457A-15
C 60	12.4	88.6	1029	2	US-08-553-943-15
C 61	12.4	88.6	1029	7	PCT-US91-09437-15
C 62	12.4	88.6	1107	3	US-09-270-767-13779
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C 94	12.4	88.6	4550	3	US-09-338-907-182
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c 100	12.4	88.6	10024	4	US-09-880-107-2430	Sequence 2430, Ap	173	12.4	88.6	818128	3	US-09-949-016-14547	Sequence 14547, A
c 101	12.4	88.6	11831	3	US-08-961-527-65	Sequence 65, Appl	174	12.4	88.6	818128	3	US-09-949-016-14548	Sequence 14548, A
c 102	12.4	88.6	12665	3	US-09-949-016-16388	Sequence 16388, A	175	12.4	88.6	818128	3	US-09-949-016-14548	Sequence 14548, A
c 103	12.4	88.6	15273	3	US-09-949-016-12356	Sequence 12356, A	176	12.4	88.6	818128	3	US-09-949-016-14549	Sequence 14549, A
c 104	12.4	88.6	15273	3	US-09-949-016-13341	Sequence 13341, A	177	12.4	88.6	818128	3	US-09-949-016-14549	Sequence 14549, A
c 105	12.4	88.6	17844	5	US-09-543-679A-2925	Sequence 2925, Ap	178	12.4	88.6	818128	3	US-09-949-016-14550	Sequence 14550, A
c 106	12.4	88.6	19062	3	US-09-949-016-14877	Sequence 14877, A	179	12.4	88.6	818128	3	US-09-949-016-14550	Sequence 14550, A
c 107	12.4	88.6	22071	3	US-09-949-016-15458	Sequence 15458, A	180	12.4	88.6	818128	3	US-09-949-016-14551	Sequence 14551, A
c 108	12.4	88.6	23445	3	US-09-949-016-12955	Sequence 12955, A	181	12.4	88.6	818128	3	US-09-949-016-14551	Sequence 14551, A
c 109	12.4	88.6	36759	3	US-09-949-016-12216	Sequence 12216, A	182	12.4	88.6	818128	3	US-09-949-016-14552	Sequence 14552, A
c 110	12.4	88.6	36760	3	US-09-949-016-14021	Sequence 14021, A	183	12.4	88.6	818128	3	US-09-949-016-14552	Sequence 14552, A
c 111	12.4	88.6	38920	3	US-09-949-016-17546	Sequence 17546, A	184	12.4	88.6	818128	3	US-09-949-016-14553	Sequence 14553, A
c 112	12.4	88.6	39003	3	US-09-596-002-21	Sequence 21, Appl	185	12.4	88.6	818128	3	US-09-949-016-14553	Sequence 14553, A
c 113	12.4	88.6	40147	3	US-09-949-016-12374	Sequence 12374, A	186	12.4	88.6	818128	3	US-09-949-016-14554	Sequence 14554, A
c 114	12.4	88.6	40379	3	US-09-949-016-14128	Sequence 14128, A	187	12.4	88.6	818128	3	US-09-949-016-14554	Sequence 14554, A
c 115	12.4	88.6	40877	3	US-09-949-016-17495	Sequence 17495, A	188	12.4	88.6	818128	3	US-09-949-016-14555	Sequence 14555, A
c 116	12.4	88.6	47419	3	US-09-949-016-11841	Sequence 11841, A	189	12.4	88.6	818128	3	US-09-949-016-14555	Sequence 14555, A
c 117	12.4	88.6	47420	3	US-09-949-016-15484	Sequence 15484, A	190	12.4	88.6	818128	3	US-09-949-016-14556	Sequence 14556, A
c 118	12.4	88.6	47476	3	US-09-949-016-12179	Sequence 12179, A	191	12.4	88.6	818128	3	US-09-949-016-14556	Sequence 14556, A
c 119	12.4	88.6	47476	3	US-09-949-016-14472	Sequence 14472, A	192	12.4	88.6	818128	3	US-09-949-016-14557	Sequence 14557, A
c 120	12.4	88.6	50000	3	US-09-146-053-3	Sequence 3, Appli	193	12.4	88.6	818128	3	US-09-949-016-14557	Sequence 14557, A
c 121	12.4	88.6	70383	3	US-10-283-247-3	Sequence 3, Appli	194	12.4	88.6	818128	3	US-09-949-016-14558	Sequence 14558, A
c 122	12.4	88.6	76553	3	US-09-949-016-13432	Sequence 13432, A	195	12.4	88.6	818128	3	US-09-949-016-14558	Sequence 14558, A
c 123	12.4	88.6	86639	3	US-09-949-016-17397	Sequence 17397, A	196	12.4	88.6	818128	3	US-09-949-016-14559	Sequence 14559, A
c 124	12.4	88.6	86936	3	US-09-949-016-17314	Sequence 17314, A	197	12.4	88.6	818128	3	US-09-949-016-14559	Sequence 14559, A
c 125	12.4	88.6	91931	3	US-09-949-016-13694	Sequence 13694, A	198	12.4	88.6	818128	3	US-09-949-016-14560	Sequence 14560, A
c 126	12.4	88.6	92304	3	US-09-949-016-15943	Sequence 15943, A	199	12.4	88.6	818128	3	US-09-949-016-14560	Sequence 14560, A
c 127	12.4	88.6	92387	3	US-09-949-016-14563	Sequence 14563, A	200	12.4	88.6	818128	3	US-09-949-016-14561	Sequence 14561, A
c 128	12.4	88.6	94156	3	US-09-949-016-12388	Sequence 12388, A	201	12.4	88.6	818128	3	US-09-949-016-14561	Sequence 14561, A
c 129	12.4	88.6	100877	3	US-09-949-016-13276	Sequence 13276, A	202	12.4	88.6	818128	3	US-09-949-016-14562	Sequence 14562, A
c 130	12.4	88.6	102406	3	US-09-949-016-14673	Sequence 14673, A	203	12.4	88.6	818128	3	US-09-949-016-14562	Sequence 14562, A
c 131	12.4	88.6	106399	3	US-09-949-016-12393	Sequence 12393, A	204	12.4	88.6	818128	3	US-09-949-016-14564	Sequence 14564, A
c 132	12.4	88.6	119930	3	US-09-949-016-12677	Sequence 12677, A	205	12.4	88.6	818128	3	US-09-949-016-14565	Sequence 14565, A
c 133	12.4	88.6	119931	3	US-09-949-016-16319	Sequence 16319, A	206	12.4	88.6	818128	3	US-09-949-016-14565	Sequence 14565, A
c 134	12.4	88.6	125936	3	US-09-949-016-14186	Sequence 14186, A	207	12.4	88.6	818128	3	US-09-949-016-14565	Sequence 14565, A
c 135	12.4	88.6	129899	3	US-09-949-016-14684	Sequence 14684, A	208	12.4	88.6	818128	3	US-09-949-016-14566	Sequence 14566, A
c 136	12.4	88.6	134140	3	US-09-949-016-12672	Sequence 12672, A	209	12.4	88.6	818128	3	US-09-949-016-14566	Sequence 14566, A
c 137	12.4	88.6	134241	3	US-09-949-016-12424	Sequence 12424, A	210	12.4	88.6	818128	3	US-09-949-016-14567	Sequence 14567, A
c 138	12.4	88.6	134242	3	US-09-949-016-15813	Sequence 15813, A	211	12.4	88.6	818128	3	US-09-949-016-14567	Sequence 14567, A
c 139	12.4	88.6	134242	3	US-09-949-016-15814	Sequence 15814, A	212	12.4	88.6	12300235	3	US-09-138-452A-1	Sequence 1, Appli
c 140	12.4	88.6	134242	3	US-09-949-016-15815	Sequence 15815, A	213	12.4	88.6	12300235	3	US-09-138-452A-1	Sequence 1, Appli
c 141	12.4	88.6	145241	3	US-09-949-016-17394	Sequence 17394, A	214	12	85.7	50	4	US-10-093-322-312	Sequence 312, App
c 142	12.4	88.6	145241	3	US-09-949-016-17395	Sequence 17395, A	215	12	85.7	20	3	US-10-131-827-5884	Sequence 5884, Ap
c 143	12.4	88.6	148156	3	US-09-949-016-11776	Sequence 11776, A	216	12	85.7	255	5	US-10-131-831-5684	Sequence 5684, Ap
c 144	12.4	88.6	151295	3	US-09-949-016-14568	Sequence 14568, A	217	12	85.7	296	3	US-09-543-681A-1062	Sequence 1062, Ap
c 145	12.4	88.6	151295	3	US-09-949-016-14568	Sequence 14568, A	218	12	85.7	324	4	US-09-533-559-3373	Sequence 2373, Ap
c 146	12.4	88.6	151295	3	US-09-949-016-14569	Sequence 14569, A	219	12	85.7	330	3	US-09-880-107-991	Sequence 981, App
c 147	12.4	88.6	151295	3	US-09-949-016-14569	Sequence 14569, A	220	12	85.7	384	4	US-09-134-001C-686	Sequence 686, App
c 148	12.4	88.6	151295	3	US-09-949-016-14570	Sequence 14570, A	221	12	85.7	601	3	US-09-605-703B-2423	Sequence 2423, Ap
c 149	12.4	88.6	151295	3	US-09-949-016-14570	Sequence 14570, A	222	12	85.7	601	3	US-09-949-016-30474	Sequence 30474, A
c 150	12.4	88.6	151295	3	US-09-949-016-14571	Sequence 14571, A	223	12	85.7	601	3	US-09-949-016-38992	Sequence 38992, A
c 151	12.4	88.6	151295	3	US-09-949-016-14571	Sequence 14571, A	224	12	85.7	601	3	US-09-949-016-38993	Sequence 38993, A
c 152	12.4	88.6	151295	3	US-09-949-016-14572	Sequence 14572, A	225	12	85.7	601	3	US-09-949-016-38994	Sequence 38994, A
c 153	12.4	88.6	151295	3	US-09-949-016-14572	Sequence 14572, A	226	12	85.7	601	3	US-09-949-016-38995	Sequence 38995, A
c 154	12.4	88.6	178883	3	US-09-949-016-12733	Sequence 12733, A	227	12	85.7	601	3	US-09-949-016-45510	Sequence 45510, A
c 155	12.4	88.6	178884	3	US-09-949-016-13039	Sequence 13039, A	228	12	85.7	601	3	US-09-949-016-65383	Sequence 65383, A
c 156	12.4	88.6	187580	3	US-09-949-016-13266	Sequence 13266, A	229	12	85.7	601	3	US-09-949-016-94881	Sequence 94881, A
c 157	12.4	88.6	189842	3	US-09-949-016-13209	Sequence 13209, A	230	12	85.7	601	3	US-09-949-016-94882	Sequence 94882, A
c 158	12.4	88.6	228896	3	US-09-949-016-17127	Sequence 17127, A	231	12	85.7	601	3	US-09-949-016-94897	Sequence 94897, A
c 159	12.4	88.6	245286	3	US-09-949-016-15497	Sequence 15497, A	232	12	85.7	601	3	US-09-949-016-94898	Sequence 94898, A
c 160	12.4	88.6	253375	3	US-09-949-016-12849	Sequence 12849, A	233	12	85.7	601	3	US-09-949-016-128760	Sequence 128760, A
c 161	12.4	88.6	298336	3	US-09-949-016-16600	Sequence 16600, A	234	12	85.7	601	3	US-09-949-016-136166	Sequence 136166, A
c 162	12.4	88.6	392000	3	US-10-027-983-11	Sequence 11, Appl	235	12	85.7	601	3	US-09-949-016-140032	Sequence 140032, A
c 163	12.4	88.6	393753	3	US-09-949-016-14573	Sequence 14573, A	236	12	85.7	601	3	US-09-949-016-140033	Sequence 140033, A
c 164	12.4	88.6	393753	3	US-09-949-016-14573	Sequence 14573, A	237	12	85.7	601	3	US-09-949-016-140048	Sequence 140048, A
c 165	12.4	88.6	393753	3	US-09-949-016-14574	Sequence 14574, A	238	12	85.7	601	3	US-09-949-016-140049	Sequence 140049, A
c 166	12.4	88.6	393753	3	US-09-949-016-14574	Sequence 14574, A	239	12	85.7	601	3	US-09-949-016-144986	Sequence 144986, A
c 167	12.4	88.6	611587	4	US-09-531-120-209	Sequence 209, App	240	12	85.7	601	3	US-09-949-016-178958	Sequence 178958, A
c 168	12.4	88.6	670689	3	US-09-949-016-12505	Sequence 12505, A	241	12	85.7	601	3	US-09-949-016-178959	Sequence 178959, A
c 169	12.4	88.6	670690	3	US-09-949-016-14207	Sequence 14207, A	242	12	85.7	601	3	US-09-949-016-178960	Sequence 178960, A

243	12	85.7	601	3	US-09-949-016-178961	Sequence 178961,	c 316	12	85.7	58812	3	US-09-949-016-17197	Sequence 17197,
244	12	85.7	601	3	US-09-949-016-192350	Sequence 192350,	317	12	85.7	69701	3	US-09-949-016-14187	Sequence 14187,
245	12	85.7	601	3	US-09-949-016-196978	Sequence 196978,	318	12	85.7	73308	3	US-09-949-016-163326	Sequence 16326,
246	12	85.7	601	3	US-09-949-016-202053	Sequence 202053,	c 319	12	85.7	74804	3	US-09-949-016-15118	Sequence 15118,
247	12	85.7	601	3	US-09-949-016-202054	Sequence 202054,	320	12	85.7	77851	3	US-09-949-016-125508	Sequence 12508,
248	12	85.7	768	3	US-09-540-236-909	Sequence 909, App	321	12	85.7	77867	3	US-09-949-016-13211	Sequence 13211,
249	12	85.7	843	3	US-09-328-32-1259	Sequence 1259, App	322	12	85.7	77867	3	US-09-949-016-13212	Sequence 13212,
250	12	85.7	861	3	US-09-902-540-4130	Sequence 4130, Ap	323	12	85.7	77940	3	US-09-949-016-12509	Sequence 12509,
251	12	85.7	861	4	US-10-099-322-321	Sequence 321, App	324	12	85.7	83938	3	US-09-949-016-16068	Sequence 16068,
252	12	85.7	877	3	US-09-636-215-769	Sequence 769, App	325	12	85.7	83968	3	US-09-949-016-12025	Sequence 12025,
253	12	85.7	877	3	US-09-685-166A-769	Sequence 769, App	326	12	85.7	90544	3	US-09-949-016-13302	Sequence 13302,
254	12	85.7	877	3	US-09-679-426-769	Sequence 769, App	327	12	85.7	95566	3	US-09-949-016-11877	Sequence 11877,
255	12	85.7	877	3	US-09-759-143-769	Sequence 769, App	328	12	85.7	99370	3	US-09-949-016-12816	Sequence 12816,
256	12	85.7	877	3	US-09-651-236-769	Sequence 769, App	329	12	85.7	99370	3	US-09-949-016-17540	Sequence 17540,
257	12	85.7	877	3	US-09-657-279-769	Sequence 769, App	330	12	85.7	101894	3	US-09-949-016-12505	Sequence 12505,
258	12	85.7	877	3	US-10-012-896A-769	Sequence 769, App	331	12	85.7	103894	3	US-09-949-016-14450	Sequence 14450,
259	12	85.7	877	3	US-10-144-678A-769	Sequence 769, App	332	12	85.7	105168	3	US-09-949-016-13296	Sequence 13296,
260	12	85.7	929	3	US-09-533-559-7620	Sequence 7620, Ap	333	12	85.7	126237	3	US-09-949-016-16674	Sequence 16674,
261	12	85.7	1072	3	US-09-902-540-3303	Sequence 3303, Ap	334	12	85.7	126237	3	US-09-949-016-16675	Sequence 16675,
262	12	85.7	1170	5	US-09-974-300-1705	Sequence 1705, Ap	335	12	85.7	128273	3	US-09-949-016-17533	Sequence 17533,
263	12	85.7	1192	4	US-10-099-322-17	Sequence 17, Appl	336	12	85.7	143155	3	US-09-949-016-11925	Sequence 11925,
264	12	85.7	1192	4	US-09-880-107-3409	Sequence 3409, Ap	337	12	85.7	143164	3	US-09-949-016-14368	Sequence 14368,
265	12	85.7	1192	4	US-10-044-564-17	Sequence 17, Appl	338	12	85.7	143173	3	US-09-949-016-14513	Sequence 14513,
266	12	85.7	1245	3	US-09-354-123-7	Sequence 7, Appl	339	12	85.7	152331	3	US-09-128-155-16	Sequence 15, Appl
267	12	85.7	1260	3	US-09-328-352-272	Sequence 272, App	340	12	85.7	153642	3	US-09-949-016-12174	Sequence 12174,
268	12	85.7	1503	4	US-09-605-703B-1765	Sequence 1765, Ap	341	12	85.7	153642	3	US-09-949-016-12174	Sequence 12174,
269	12	85.7	1840	3	US-09-620-312D-320	Sequence 320, App	c 342	12	85.7	153643	3	US-09-949-016-15635	Sequence 1

C 389	11.4	81.4	370	3	US-09-124-523-49	Sequence 49, Appl	462	11.4	81.4	601	3	US-09-949-016-21974	Sequence 21974, A
C 390	11.4	81.4	370	3	US-09-636-796A-49	Sequence 49, Appl	463	11.4	81.4	601	3	US-09-949-016-21975	Sequence 21975, A
C 391	11.4	81.4	370	3	US-08-431-048P-49	Sequence 49, Appl	464	11.4	81.4	601	3	US-09-949-016-23862	Sequence 23862, A
C 392	11.4	81.4	372	4	US-09-689-159A-49	Sequence 49, Appl	465	11.4	81.4	601	3	US-09-949-016-24740	Sequence 24740, A
C 393	11.4	81.4	377	2	US-08-967-101-53	Sequence 53, Appl	466	11.4	81.4	601	3	US-09-949-016-26718	Sequence 26718, A
C 394	11.4	81.4	377	2	US-08-962-541-53	Sequence 53, Appl	467	11.4	81.4	601	3	US-09-949-016-26846	Sequence 26846, A
C 395	11.4	81.4	377	3	US-09-124-698-53	Sequence 53, Appl	c 468	11.4	81.4	601	3	US-09-949-016-27104	Sequence 27104, A
C 396	11.4	81.4	377	3	US-09-127-480-53	Sequence 53, Appl	c 469	11.4	81.4	601	3	US-09-949-016-27105	Sequence 27105, A
C 397	11.4	81.4	377	3	US-08-496-841C-53	Sequence 53, Appl	c 470	11.4	81.4	601	3	US-09-949-016-29345	Sequence 29345, A
C 398	11.4	81.4	377	3	US-09-124-523-53	Sequence 53, Appl	c 471	11.4	81.4	601	3	US-09-949-016-29346	Sequence 29346, A
C 399	11.4	81.4	377	3	US-09-636-796A-53	Sequence 53, Appl	c 472	11.4	81.4	601	3	US-09-949-016-29347	Sequence 29347, A
C 400	11.4	81.4	377	3	US-08-431-048P-53	Sequence 53, Appl	c 473	11.4	81.4	601	3	US-09-949-016-29874	Sequence 29874, A
C 401	11.4	81.4	380	4	US-09-689-159A-53	Sequence 53, Appl	474	11.4	81.4	601	3	US-09-949-016-36304	Sequence 36304, A
c 402	11.4	81.4	386	2	US-08-967-101-52	Sequence 52, Appl	475	11.4	81.4	601	3	US-09-949-016-36305	Sequence 36305, A
403	11.4	81.4	386	2	US-08-592-541-52	Sequence 52, Appl	476	11.4	81.4	601	3	US-09-949-016-39834	Sequence 39834, A
404	11.4	81.4	386	3	US-09-124-698-52	Sequence 52, Appl	477	11.4	81.4	601	3	US-09-949-016-39835	Sequence 39835, A
405	11.4	81.4	386	3	US-09-127-480-52	Sequence 52, Appl	c 478	11.4	81.4	601	3	US-09-949-016-40052	Sequence 40052, A
406	11.4	81.4	386	3	US-08-496-841C-52	Sequence 52, Appl	c 479	11.4	81.4	601	3	US-09-949-016-44887	Sequence 44887, A
407	11.4	81.4	386	3	US-09-124-523-52	Sequence 52, Appl	c 480	11.4	81.4	601	3	US-09-949-016-44888	Sequence 44888, A
408	11.4	81.4	386	3	US-09-636-796A-52	Sequence 52, Appl	c 481	11.4	81.4	601	3	US-09-949-016-44889	Sequence 44889, A
409	11.4	81.4	387	4	US-08-431-048P-52	Sequence 52, Appl	c 482	11.4	81.4	601	3	US-09-949-016-48133	Sequence 48133, A
410	11.4	81.4	387	4	US-09-689-159A-52	Sequence 52, Appl	c 483	11.4	81.4	601	3	US-09-949-016-48340	Sequence 48340, A
411	11.4	81.4	390	3	US-09-107-532A-775	Sequence 52, Appl	c 484	11.4	81.4	601	3	US-09-949-016-48840	Sequence 48840, A
412	11.4	81.4	390	3	US-09-489-039A-3791	Sequence 3791, App	485	11.4	81.4	601	3	US-09-949-016-48841	Sequence 48841, A
c 413	11.4	81.4	400	3	US-09-513-999C-10479	Sequence 10479, A	486	11.4	81.4	601	3	US-09-949-016-49012	Sequence 49012, A
c 414	11.4	81.4	409	3	US-09-270-767-2687	Sequence 2687, Ap	487	11.4	81.4	601	3	US-09-949-016-49013	Sequence 49013, A
c 415	11.4	81.4	409	3	US-09-270-767-17969	Sequence 17969, A	488	11.4	81.4	601	3	US-09-949-016-49184	Sequence 49184, A
416	11.4	81.4	440	2	US-08-967-101-58	Sequence 58, Appl	489	11.4	81.4	601	3	US-09-949-016-49185	Sequence 49185, A
417	11.4	81.4	440	2	US-08-592-541-58	Sequence 58, Appl	490	11.4	81.4	601	3	US-09-949-016-49360	Sequence 49360, A
418	11.4	81.4	440	3	US-09-124-698-58	Sequence 58, Appl	491	11.4	81.4	601	3	US-09-949-016-49361	Sequence 49361, A
419	11.4	81.4	440	3	US-09-127-480-58	Sequence 58, Appl	492	11.4	81.4	601	3	US-09-949-016-50840	Sequence 50840, A
420	11.4	81.4	440	3	US-08-496-841C-58	Sequence 58, Appl	493	11.4	81.4	601	3	US-09-949-016-50841	Sequence 50841, A
421	11.4	81.4	440	3	US-09-124-523-58	Sequence 58, Appl	494	11.4	81.4	601	3	US-09-949-016-55841	Sequence 55841, A
422	11.4	81.4	440	3	US-09-636-796A-58	Sequence 58, Appl	495	11.4	81.4	601	3	US-09-949-016-56953	Sequence 56953, A
423	11.4	81.4	440	3	US-08-431-048P-58	Sequence 58, Appl	496	11.4	81.4	601	3	US-09-949-016-58317	Sequence 58317, A
424	11.4	81.4	440	4	US-09-689-159A-58	Sequence 58, Appl	497	11.4	81.4	601	3	US-09-949-016-58643	Sequence 58643, A
425	11.4	81.4	442	3	US-09-270-767-3123	Sequence 3123, Ap	c 498	11.4	81.4	601	3	US-09-949-016-64188	Sequence 64188, A
426	11.4	81.4	442	3	US-09-270-767-18405	Sequence 18405, A	c 499	11.4	81.4	601	3	US-09-949-016-65475	Sequence 65475, A
c 427	11.4	81.4	446	3	US-09-621-976-13229	Sequence 13229, A	c 500	11.4	81.4	601	3	US-09-949-016-65476	Sequence 65476, A
428	11.4	81.4	457	3	US-09-621-976-11119	Sequence 11119, A	c 501	11.4	81.4	601	3	US-09-949-016-73793	Sequence 73793, A
c 429	11.4	81.4	465	3	US-09-489-039A-3756	Sequence 3756, Ap	c 502	11.4	81.4	601	3	US-09-949-016-77692	Sequence 77692, A
c 430	11.4	81.4	468	3	US-09-270-767-1802	Sequence 1802, Ap	c 503	11.4	81.4	601	3	US-09-949-016-84295	Sequence 84295, A
c 431	11.4	81.4	468	3	US-09-270-767-17084	Sequence 17084, A	504	11.4	81.4	601	3	US-09-949-016-84296	Sequence 84296, A
432	11.4	81.4	477	3	US-09-313-294A-4870	Sequence 4870, Ap	c 505	11.4	81.4	601	3	US-09-949-016-85739	Sequence 85739, A
433	11.4	81.4	482	3	US-09-270-767-8390	Sequence 8390, Ap	506	11.4	81.4	601	3	US-09-949-016-86581	Sequence 86581, A
434	11.4	81.4	482	3	US-09-270-767-23672	Sequence 23672, A	507	11.4	81.4	601	3	US-09-949-016-86582	Sequence 86582, A
c 435	11.4	81.4	483	3	US-09-621-976-9241	Sequence 9241, Ap	508	11.4	81.4	601	3	US-09-949-016-103340	Sequence 103340, A
c 436	11.4	81.4	493	3	US-09-533-559-1725	Sequence 1725, Ap	509	11.4	81.4	601	3	US-09-949-016-103341	Sequence 103341, A
c 437	11.4	81.4	498	3	US-09-621-976-17779	Sequence 17779, Ap	510	11.4	81.4	601	3	US-09-949-016-107463	Sequence 107463, A
438	11.4	81.4	501	5	US-09-974-300-6752	Sequence 6752, Ap	511	11.4	81.4	601	3	US-09-949-016-107532	Sequence 107532, A
439	11.4	81.4	503	3	US-09-621-976-16499	Sequence 16499, A	c 512	11.4	81.4	601	3	US-09-949-016-112286	Sequence 112286, A
440	11.4	81.4	503	3	US-09-621-976-16500	Sequence 16500, A	513	11.4	81.4	601	3	US-09-949-016-120053	Sequence 120053, A
441	11.4	81.4	503	3	US-09-621-976-16501	Sequence 16501, A	514	11.4	81.4	601	3	US-09-949-016-120103	Sequence 120103, A
c 442	11.4	81.4	504	3	US-09-540-236-1375	Sequence 1375, Ap	515	11.4	81.4	601	3	US-09-949-016-120153	Sequence 120153, A
c 443	11.4	81.4	509	3	US-09-880-107-110	Sequence 110, App	c 516	11.4	81.4	601	3	US-09-949-016-121518	Sequence 121518, A
444	11.4	81.4	513	4	US-09-621-976-16497	Sequence 16497, A	517	11.4	81.4	601	3	US-09-949-016-121894	Sequence 121894, A
c 445	11.4	81.4	526	3	US-09-513-999C-15677	Sequence 15677, A	518	11.4	81.4	601	3	US-09-949-016-132449	Sequence 132449, A
c 446	11.4	81.4	528	3	US-09-949-016-3093	Sequence 3093, Ap	519	11.4	81.4	601	3	US-09-949-016-132450	Sequence 132450, A
c 447	11.4	81.4	529	3	US-09-949-016-2262	Sequence 2262, Ap	c 520	11.4	81.4	601	3	US-09-949-016-137703	Sequence 137703, A
c 448	11.4	81.4	531	4	US-09-880-107-137	Sequence 137, App	c 521	11.4	81.4	601	3	US-09-949-016-137704	Sequence 137704, A
c 449	11.4	81.4	535	3	US-09-770-509-1	Sequence 1, Appl	c 522	11.4	81.4	601	3	US-09-949-016-139624	Sequence 139624, A
450	11.4	81.4	540	3	US-09-489-039A-156	Sequence 156, App	c 523	11.4	81.4	601	3	US-09-949-016-140832	Sequence 140832, A
451	11.4	81.4	541	3	US-09-270-767-5356	Sequence 5356, Ap	524	11.4	81.4	601	3	US-09-949-016-140838	Sequence 140838, A
c 452	11.4	81.4	541	3	US-09-270-767-20638	Sequence 20638, A	525	11.4	81.4	601	3	US-09-949-016-144399	Sequence 144399, A
c 453	11.4	81.4	547	3	US-09-270-767-25948	Sequence 25948, A	c 526	11.4	81.4	601	3	US-09-949-016-144768	Sequence 144768, A
c 454	11.4	81.4	550	3	US-08-998-416-148	Sequence 148, App	527	11.4	81.4	601	3	US-09-949-016-145276	Sequence 145276, A
c 455	11.4	81.4	558	3	US-09-489-039A-6933	Sequence 6933, Ap	c 528	11.4	81.4	601	3	US-09-949-016-146976	Sequence 146976, A
c 456	11.4	81.4	582	5	US-09-974-300-5347	Sequence 5347, Ap	c 529	11.4	81.4	601	3	US-09-949-016-148435	Sequence 148435, A
c 457	11.4	81.4	584	5	US-09-974-300-608	Sequence 608, App	c 530	11.4	81.4	601	3	US-09-949-016-148436	Sequence 148436, A
c 458	11.4	81.4	586	3	US-09-533-559-1738	Sequence 1738, Ap	531	11.4	81.4	601	3	US-09-949-016-149361	Sequence 149361, A
c 459	11.4	81.4	588	5	US-09-974-300-4576	Sequence 4576, Ap	532	11.4	81.4	601	3	US-09-949-016-149814	Sequence 149814, A
c 460	11.4	81.4	593	5	US-09-974-300-4874	Sequence 4874, Ap	533	11.4	81.4	601	3	US-09-949-016-155938	Sequence 155938, A
461	11.4	81.4	601	3	US-09-949-016-18973	Sequence 18973, A	534	11.4	81.4	601	3	US-09-949-016-156091	Sequence 156091, A

535	11.4	81.4	601	3	US-09-949-016-157962	Sequence 157962,	c 608	11.4	81.4	859	3	US-09-044-604-2	Sequence 2, Appli
536	11.4	81.4	601	3	US-09-949-016-157963	Sequence 157963,	c 609	11.4	81.4	864	3	US-09-270-767-10692	Sequence 10692, A
c 537	11.4	81.4	601	3	US-09-949-016-160683	Sequence 160683,	610	11.4	81.4	873	3	US-09-513-990C-8465	Sequence 8465, Ap
538	11.4	81.4	601	3	US-09-949-016-160857	Sequence 160857,	611	11.4	81.4	882	3	US-09-949-016-3413	Sequence 3413, Ap
539	11.4	81.4	601	3	US-09-949-016-160858	Sequence 160858,	612	11.4	81.4	885	3	US-09-489-0039A-5254	Sequence 5254, Ap
540	11.4	81.4	601	3	US-09-949-016-163274	Sequence 163274,	613	11.4	81.4	905	3	US-09-602-787A-325	Sequence 325, App
541	11.4	81.4	601	3	US-09-949-016-163275	Sequence 163275,	614	11.4	81.4	906	5	US-09-974-300-2335	Sequence 2335, Ap
c 542	11.4	81.4	601	3	US-09-949-016-185298	Sequence 165298,	c 615	11.4	81.4	924	3	US-09-991-181-508	Sequence 508, App
543	11.4	81.4	601	3	US-09-949-016-166376	Sequence 166376,	c 616	11.4	81.4	924	3	US-09-990-444-508	Sequence 508, App
544	11.4	81.4	601	3	US-09-949-016-169123	Sequence 169123,	c 617	11.4	81.4	924	3	US-09-997-333-508	Sequence 508, App
545	11.4	81.4	601	3	US-09-949-016-171724	Sequence 171724,	c 618	11.4	81.4	924	3	US-09-992-598-508	Sequence 508, App
c 546	11.4	81.4	601	3	US-09-949-016-172455	Sequence 172455,	c 619	11.4	81.4	924	4	US-09-989-735-508	Sequence 508, App
547	11.4	81.4	601	3	US-09-949-016-172547	Sequence 172547,	c 620	11.4	81.4	924	5	US-09-989-726-508	Sequence 508, App
548	11.4	81.4	601	3	US-09-949-016-172548	Sequence 172548,	c 621	11.4	81.4	924	5	US-09-997-514-508	Sequence 508, App
549	11.4	81.4	601	3	US-09-949-016-172549	Sequence 172549,	c 622	11.4	81.4	924	5	US-09-989-728-508	Sequence 508, App
c 550	11.4	81.4	601	3	US-09-949-016-173810	Sequence 173810,	c 623	11.4	81.4	924	5	US-09-997-349-508	Sequence 508, App
c 551	11.4	81.4	601	3	US-09-949-016-173811	Sequence 173811,	c 624	11.4	81.4	924	5	US-09-997-653-508	Sequence 508, App
c 552	11.4	81.4	601	3	US-09-949-016-173812	Sequence 173812,	c 625	11.4	81.4	924	5	US-09-989-293A-508	Sequence 508, App
c 553	11.4	81.4	601	3	US-09-949-016-174970	Sequence 174970,	c 626	11.4	81.4	939	3	US-09-949-002-113	Sequence 113, App
c 554	11.4	81.4	601	3	US-09-949-016-174983	Sequence 174983,	c 627	11.4	81.4	948	3	US-09-248-796A-1474	Sequence 1474, Ap
c 555	11.4	81.4	601	3	US-09-949-016-174996	Sequence 174996,	c 628	11.4	81.4	966	2	US-08-921-382-1	Sequence 1, Appli
c 556	11.4	81.4	601	3	US-09-949-016-179438	Sequence 179438,	c 629	11.4	81.4	966	3	US-09-386-380-1	Sequence 1, Appli
c 557	11.4	81.4	601	3	US-09-949-016-179439	Sequence 179439,	c 630	11.4	81.4	991	3	US-09-149-476-175	Sequence 175, App
c 558	11.4	81.4	601	3	US-09-949-016-179447	Sequence 179447,	631	11.4	81.4	1001	3	US-09-641-638-260	Sequence 260, App
c 559	11.4	81.4	601	3	US-09-949-016-181312	Sequence 181312,	632	11.4	81.4	1001	3	US-09-671-317-427	Sequence 427, App
c 560	11.4	81.4	601	3	US-09-949-016-181349	Sequence 181349,	633	11.4	81.4	1001	3	US-10-170-097-260	Sequence 260, App
c 561	11.4	81.4	601	3	US-09-949-016-181386	Sequence 181386,	634	11.4	81.4	1008	3	US-09-533-553-2485	Sequence 2485, Ap
c 562	11.4	81.4	601	3	US-09-949-016-181632	Sequence 181632,	635	11.4	81.4	1020	3	US-09-710-279-1693	Sequence 1693, Ap
563	11.4	81.4	601	3	US-09-949-016-184495	Sequence 184495,	636	11.4	81.4	1038	2	US-08-134-570-13	Sequence 13, Appl
564	11.4	81.4	601	3	US-09-949-016-184496	Sequence 184496,	637	11.4	81.4	1041	3	US-09-134-001C-2359	Sequence 2359, Ap
565	11.4	81.4	601	3	US-09-949-016-184497	Sequence 184497,	638	11.4	81.4	1053	3	US-09-248-796A-5854	Sequence 5854, Ap
566	11.4	81.4	601	3	US-09-949-016-184932	Sequence 184932,	639	11.4	81.4	1059	3	US-09-328-352-2355	Sequence 2355, Ap
c 567	11.4	81.4	601	3	US-09-949-016-188302	Sequence 188302,	640	11.4	81.4	1074	3	US-09-543-681A-854	Sequence 854, App
c 568	11.4	81.4	601	3	US-09-949-016-188367	Sequence 188367,	641	11.4	81.4	1088	5	US-09-974-300-703	Sequence 703, App
c 569	11.4	81.4	601	3	US-09-949-016-188368	Sequence 188368,	642	11.4	81.4	1107	3	US-09-614-221A-61	Sequence 61, Appl
c 570	11.4	81.4	601	3	US-09-949-016-194160	Sequence 194160,	643	11.4	81.4	1122	3	US-09-270-767-10529	Sequence 10529, A
571	11.4	81.4	601	3	US-09-949-016-197805	Sequence 197805,	644	11.4	81.4	1160	3	US-09-153-310-41	Sequence 41, Appl
572	11.4	81.4	601	3	US-09-949-016-197852	Sequence 197852,	645	11.4	81.4	1185	3	US-09-248-796A-6620	Sequence 6620, Ap
c 573	11.4	81.4	601	3	US-09-949-016-198633	Sequence 198633,	646	11.4	81.4	1188	3	US-09-362-842-5	Sequence 5, Appli
c 574	11.4	81.4	601	3	US-09-949-016-198634	Sequence 198634,	647	11.4	81.4	1218	3	US-09-328-352-223	Sequence 223, App
c 575	11.4	81.4	601	3	US-09-949-016-202835	Sequence 202835,	648	11.4	81.4	1248	3	US-09-902-540-2311	Sequence 2311, Ap
c 576	11.4	81.4	601	3	US-09-949-016-204054	Sequence 204054,	c 649	11.4	81.4	1251	2	US-08-851-088-5	Sequence 5, Appli
c 577	11.4	81.4	601	3	US-09-949-016-204055	Sequence 204055,	c 650	11.4	81.4	1259	3	US-09-902-540-88	Sequence 88, Appl
c 578	11.4	81.4	601	3	US-09-949-016-204056	Sequence 204056,	c 651	11.4	81.4	1266	3	US-09-328-352-3014	Sequence 3014, Ap
c 579	11.4	81.4	601	3	US-09-949-016-204863	Sequence 204863,	652	11.4	81.4	1313	3	US-09-035-648-22	Sequence 22, Appl
c 580	11.4	81.4	601	3	US-09-949-016-204864	Sequence 204864,	653	11.4	81.4	1313	3	US-09-001-951-22	Sequence 22, Appl
581	11.4	81.4	601	3	US-09-949-002-913	Sequence 913, App	654	11.4	81.4	1313	3	US-08-818-825-22	Sequence 13, Appl
c 582	11.4	81.4	601	3	US-09-949-002-914	Sequence 914, App	c 655	11.4	81.4	1328	3	US-08-930-285-13	Sequence 3, Appli
c 583	11.4	81.4	601	3	US-09-949-002-1109	Sequence 1109, Ap	c 656	11.4	81.4	1371	3	US-09-350-758-3	Sequence 1, Appli
c 584	11.4	81.4	601	3	US-09-949-002-1649	Sequence 1649, Ap	c 657	11.4	81.4	1380	3	US-09-582-779A-1	Sequence 1, Appli
c 585	11.4	81.4	601	3	US-09-949-002-3922	Sequence 3922, Ap	c 658	11.4	81.4	1386	3	US-09-543-681A-1519	Sequence 1519, Ap
c 586	11.4	81.4	601	3	US-09-949-002-5280	Sequence 5280, Ap	c 659	11.4	81.4	1419	3	US-09-270-767-30657	Sequence 30657, A
c 587	11.4	81.4	601	3	US-09-949-002-5281	Sequence 5281, Ap	c 660	11.4	81.4	1422	3	US-09-134-000C-2035	Sequence 2035, Ap
c 588	11.4	81.4	601	3	US-09-949-002-5657	Sequence 5657, Ap	c 661	11.4	81.4	1440	3	US-09-543-681A-684	Sequence 684, App
c 589	11.4	81.4	601	3	US-09-949-002-5869	Sequence 5869, Ap	c 662	11.4	81.4	1475	3	US-09-244-805-13	Sequence 13, Appl
590	11.4	81.4	606	3	US-09-918-686-9	Sequence 9, Appli	c 663	11.4	81.4	1494	3	US-09-710-279-2811	Sequence 2811, Ap
c 591	11.4	81.4	618	3	US-09-134-001C-1295	Sequence 3019, Ap	c 664	11.4	81.4	1497	3	US-09-328-352-880	Sequence 880, App
c 592	11.4	81.4	627	3	US-09-248-796A-7678	Sequence 1295, Ap	c 665	11.4	81.4	1515	3	US-09-902-540-9184	Sequence 9184, Ap
c 593	11.4	81.4	645	3	US-09-328-352-661	Sequence 7678, Ap	c 666	11.4	81.4	1534	2	US-07-973-431B-2	Sequence 2, Appli
c 594	11.4	81.4	657	3	US-09-620-312D-543	Sequence 543, App	c 667	11.4	81.4	1539	2	US-08-899-811-22	Sequence 22, Appl
c 595	11.4	81.4	675	3	US-09-328-352-2490	Sequence 2490, Ap	c 668	11.4	81.4	1608	2	US-08-424-224-1	Sequence 1, Appli
c 596	11.4	81.4	678	3	US-09-533-559-4614	Sequence 4614, Ap	c 669	11.4	81.4	1608	7	PCT-US94-02891-68	Sequence 68, Appl
c 597	11.4	81.4	684	3	US-09-134-000C-2674	Sequence 2674, Ap	c 670	11.4	81.4	1652	3	US-08-726-214-17	Sequence 17, Appl
c 598	11.4	81.4	709	4	US-09-297-648-2887	Sequence 2887, Ap	c 671	11.4	81.4	1683	3	US-09-976-594-861	Sequence 861, App
c 599	11.4	81.4	715	3	US-09-533-559-4664	Sequence 4664, Ap	c 672	11.4	81.4	1686	3	US-09-799-451-327	Sequence 327, App
c 600	11.4	81.4	742	2	US-08-966-316-2	Sequence 2, Appli	c 673	11.4	81.4	1723	2	US-08-804-699-1	Sequence 1, Appli
c 601	11.4	81.4	759	3	US-09-172-4698-1	Sequence 1, Appli	c 674	11.4	81.4	1733	3	US-09-248-796A-391	Sequence 391, App
c 602	11.4	81.4	765	4	US-09-297-648-4411	Sequence 4411, Ap	c 675	11.4	81.4	1784	2	US-08-808-931-19	Sequence 19, Appl
c 603	11.4	81.4	781	4	US-09-297-648-3565	Sequence 3565, Ap	c 676	11.4	81.4	1784	3	US-08-808-323-19	Sequence 19, Appl
c 604	11.4	81.4	840	3	US-09-724-623-37	Sequence 37, Appl	c 677	11.4	81.4	1784	3	US-09-050-603A-19	Sequence 19, Appl
c 605	11.4	81.4	840	3	US-10-288-930-37	Sequence 37, Appl	c 678	11.4	81.4	1784	3	US-09-102-420B-19	Sequence 19, Appl
c 606	11.4	81.4	858	3	US-10-002-344A-66	Sequence 66, Appl	c 679	11.4	81.4	1784	3	US-09-497-698-19	Sequence 19, Appl
c 607	11.4	81.4	858	3			c 680	11.4	81.4	1784	3	US-09-730-525-19	Sequence 19, Appl

c 681	11.4	81.4	1800	2	US-08-366-783-1	Sequence 1, Appli	754	11.4	81.4	2682	3	US-09-949-016-5604	Sequence 5604, Ap
c 682	11.4	81.4	1800	2	US-08-313-098A-1	Sequence 1, Appli	755	11.4	81.4	2688	3	US-08-458-434A-3	Sequence 3, Appli
c 683	11.4	81.4	1800	2	US-08-846-021A-1	Sequence 1, Appli	756	11.4	81.4	2690	3	US-09-949-016-238	Sequence 298, App
c 684	11.4	81.4	1800	3	US-09-897-425-1	Sequence 1, Appli	757	11.4	81.4	2695	3	US-09-927-811D-8	Sequence 8, Appli
c 685	11.4	81.4	1800	3	US-09-893-525-1	Sequence 1, Appli	c 758	11.4	81.4	2709	3	US-09-313-275A-12	Sequence 12, Appl
c 686	11.4	81.4	1854	3	US-09-724-864-29	Sequence 28, Appl	c 759	11.4	81.4	2709	3	US-09-707-167-12	Sequence 12, Appl
c 687	11.4	81.4	1859	3	US-07-861-458C-1	Sequence 1, Appli	c 760	11.4	81.4	2720	3	US-10-012-231A-11	Sequence 11, Appl
c 688	11.4	81.4	1861	3	US-10-104-047-1707	Sequence 1707, Ap	c 761	11.4	81.4	2720	3	US-10-015-389A-11	Sequence 11, Appl
c 689	11.4	81.4	1902	2	US-09-258-257-1	Sequence 1, Appli	c 762	11.4	81.4	2720	3	US-10-006-768A-11	Sequence 11, Appl
c 690	11.4	81.4	1902	2	US-09-258-371-1	Sequence 1, Appli	c 763	11.4	81.4	2720	3	US-10-015-671A-11	Sequence 11, Appl
c 691	11.4	81.4	1902	3	US-08-569-721A-1	Sequence 1, Appli	c 764	11.4	81.4	2720	3	US-10-015-393A-11	Sequence 11, Appl
c 692	11.4	81.4	1902	3	US-08-751-230-1	Sequence 1, Appli	c 765	11.4	81.4	2720	3	US-10-011-833A-11	Sequence 11, Appl
c 693	11.4	81.4	1902	3	US-09-499-082-1	Sequence 1, Appli	c 766	11.4	81.4	2720	3	US-10-006-041A-11	Sequence 11, Appl
c 694	11.4	81.4	1902	3	US-09-358-372-1	Sequence 1, Appli	c 767	11.4	81.4	2720	3	US-10-012-064A-11	Sequence 11, Appl
c 695	11.4	81.4	1902	3	US-09-532-868-1	Sequence 1, Appli	c 768	11.4	81.4	2720	3	US-10-012-752A-11	Sequence 11, Appl
c 696	11.4	81.4	1903	3	US-09-927-811D-6	Sequence 6, Appli	c 769	11.4	81.4	2720	5	US-10-011-795B-11	Sequence 11, Appl
c 697	11.4	81.4	1939	3	US-09-949-016-2082	Sequence 2082, Ap	c 770	11.4	81.4	2720	5	US-10-015-386A-11	Sequence 11, Appl
c 698	11.4	81.4	1942	3	US-09-949-016-1029	Sequence 1029, Ap	c 771	11.4	81.4	2720	5	US-10-012-121A-11	Sequence 11, Appl
c 699	11.4	81.4	1947	3	US-09-489-847-26	Sequence 26, Appl	c 772	11.4	81.4	2720	5	US-10-006-485A-11	Sequence 11, Appl
c 700	11.4	81.4	1974	3	US-08-785-455-1	Sequence 1, Appli	c 773	11.4	81.4	2720	5	US-10-006-746A-11	Sequence 11, Appl
c 701	11.4	81.4	1974	4	US-09-302-024-1	Sequence 1, Appli	c 774	11.4	81.4	2720	5	US-10-012-752A-11	Sequence 11, Appl
c 702	11.4	81.4	1998	3	US-09-280-116-222	Sequence 22, App	c 775	11.4	81.4	2720	5	US-10-017-253A-11	Sequence 11, Appl
c 703	11.4	81.4	2031	3	US-08-583-110-1598	Sequence 1598, Ap	c 776	11.4	81.4	2720	5	US-10-015-519A-11	Sequence 11, Appl
c 704	11.4	81.4	2039	4	US-09-605-703B-2207	Sequence 2207, Ap	c 777	11.4	81.4	2720	5	US-10-015-715A-11	Sequence 11, Appl
c 705	11.4	81.4	2043	3	US-09-107-433-1321	Sequence 1321, Ap	c 778	11.4	81.4	2720	5	US-10-007-236A-11	Sequence 11, Appl
c 706	11.4	81.4	2044	4	US-10-094-749-111	Sequence 111, App	c 779	11.4	81.4	2733	2	US-08-846-021A-6	Sequence 6, Appli
c 707	11.4	81.4	2061	2	US-09-258-371-9	Sequence 9, Appli	c 780	11.4	81.4	2733	3	US-09-897-425-6	Sequence 6, Appli
c 708	11.4	81.4	2061	3	US-08-751-230-9	Sequence 9, Appli	c 781	11.4	81.4	2733	3	US-09-893-525-6	Sequence 6, Appli
c 709	11.4	81.4	2061	3	US-09-499-082-9	Sequence 9, Appli	c 782	11.4	81.4	2826	3	US-10-104-047-1128	Sequence 1128, Ap
c 710	11.4	81.4	2061	3	US-09-258-372-9	Sequence 9, Appli	c 783	11.4	81.4	2916	3	US-09-814-915A-31	Sequence 31, Appl
c 711	11.4	81.4	2061	3	US-09-006-783A-2	Sequence 2, Appli	c 784	11.4	81.4	2916	3	US-09-566-921-84	Sequence 84, Appl
c 712	11.4	81.4	2061	3	US-09-159-871-1	Sequence 1, Appli	c 785	11.4	81.4	3043	3	US-09-540-236-1265	Sequence 1265, Ap
c 713	11.4	81.4	2061	3	US-09-532-868-9	Sequence 9, Appli	c 786	11.4	81.4	3066	3	US-09-086-912-1	Sequence 1, Appli
c 714	11.4	81.4	2080	3	US-10-003-392-1	Sequence 1, Appli	c 787	11.4	81.4	3066	3	US-09-203-453-1	Sequence 1, Appli
c 715	11.4	81.4	2090	4	US-10-094-749-1168	Sequence 1168, Ap	c 788	11.4	81.4	3066	3	US-09-900-236-1	Sequence 1, Appli
c 716	11.4	81.4	2098	4	US-10-094-749-1336	Sequence 1336, Ap	c 789	11.4	81.4	3066	3	US-10-256-889-1	Sequence 1, Appli
c 717	11.4	81.4	2115	2	US-08-767-026-3	Sequence 3, Appli	c 790	11.4	81.4	3066	3	US-10-439-789-1	Sequence 1, Appli
c 718	11.4	81.4	2115	3	US-09-319-275A-3	Sequence 3, Appli	c 791	11.4	81.4	3076	2	US-09-205-144-1	Sequence 11, Appl
c 719	11.4	81.4	2115	3	US-09-707-167-3	Sequence 3, Appli	c 792	11.4	81.4	3076	3	US-09-814-915A-11	Sequence 11, Appl
c 720	11.4	81.4	2136	3	US-09-949-016-2970	Sequence 2970, Ap	c 793	11.4	81.4	3116	3	US-10-104-047-434	Sequence 434, App
c 721	11.4	81.4	2136	3	US-09-949-016-2971	Sequence 2971, Ap	c 794	11.4	81.4	3138	3	US-10-144-139-15	Sequence 15, Appl
c 722	11.4	81.4	2149	2	US-08-784-651-3	Sequence 3, Appli	c 795	11.4	81.4	3165	3	US-09-949-016-160	Sequence 160, App
c 723	11.4	81.4	2157	3	US-09-540-236-833	Sequence 833, App	c 796	11.4	81.4	3215	3	US-09-710-279-3691	Sequence 3691, Ap
c 724	11.4	81.4	2161	3	US-09-254-504-10	Sequence 10, Appl	c 797	11.4	81.4	3293	3	US-09-949-016-4658	Sequence 4658, Ap
c 725	11.4	81.4	2166	3	US-08-697-826A-12	Sequence 12, Appl	c 798	11.4	81.4	3309	3	US-09-710-279-3844	Sequence 3844, Ap
c 726	11.4	81.4	2193	3	US-09-107-532B-1098	Sequence 1098, Ap	c 799	11.4	81.4	3312	3	US-09-710-279-4308	Sequence 4308, Ap
c 727	11.4	81.4	2277	3	US-09-134-001C-1751	Sequence 1751, Ap	c 800	11.4	81.4	3314	3	US-09-949-016-836	Sequence 836, App
c 728	11.4	81.4	2288	2	US-08-568-459A-5	Sequence 5, Appli	c 801	11.4	81.4	3315	3	US-09-710-279-4363	Sequence 4363, Ap
c 729	11.4	81.4	2288	2	US-08-487-826B-5	Sequence 5, Appli	c 802	11.4	81.4	3341	2	US-08-868-577-18	Sequence 18, Appl
c 730	11.4	81.4	2288	3	US-09-210-288-5	Sequence 5, Appli	c 803	11.4	81.4	3341	3	US-09-207-914-18	Sequence 1823, Ap
c 731	11.4	81.4	2288	3	US-10-153-273-5	Sequence 5, Appli	c 804	11.4	81.4	3453	3	US-09-023-655-1323	Sequence 1323, Ap
c 732	11.4	81.4	2312	3	US-09-356-806-114	Sequence 114, App	c 805	11.4	81.4	3573	3	US-09-710-279-3988	Sequence 3988, Ap
c 733	11.4	81.4	2335	3	US-10-104-047-748	Sequence 748, App	c 806	11.4	81.4	3573	3	US-09-949-016-5007	Sequence 5007, Ap
c 734	11.4	81.4	2468	2	US-07-779-049-2	Sequence 2, Appli	c 807	11.4	81.4	3585	3	US-09-270-767-14479	Sequence 14479, A
c 735	11.4	81.4	2468	2	US-08-080-240-2	Sequence 2, Appli	c 808	11.4	81.4	3624	3	US-09-328-352-2640	Sequence 2640, Ap
c 736	11.4	81.4	2499	4	US-10-094-749-207	Sequence 207, App	c 809	11.4	81.4	3729	3	US-09-710-279-3675	Sequence 3675, Ap
c 737	11.4	81.4	2517	3	US-09-712-363-4	Sequence 4, Appli	c 810	11.4	81.4	3778	3	US-09-799-451-160	Sequence 160, App
c 738	11.4	81.4	2520	3	US-09-929-612A-3	Sequence 3, Appli	c 811	11.4	81.4	3806	3	US-09-710-279-4166	Sequence 4166, App
c 739	11.4	81.4	2563	3	US-09-016-434-1076	Sequence 1076, Ap	c 812	11.4	81.4	3878	3	US-10-101-464A-950	Sequence 950, App
c 740	11.4	81.4	2563	3	US-09-023-655-894	Sequence 894, App	c 813	11.4	81.4	3888	3	US-09-897-425-42	Sequence 42, Appl
c 741	11.4	81.4	2566	4	US-10-094-749-477	Sequence 477, App	c 814	11.4	81.4	3888	3	US-09-897-425-45	Sequence 45, Appl
c 742	11.4	81.4	2601	3	US-08-569-749-3	Sequence 3, Appli	c 815	11.4	81.4	3913	3	US-09-710-279-4322	Sequence 4322, Ap
c 743	11.4	81.4	2601	3	US-09-689-366-3	Sequence 3, Appli	c 816	11.4	81.4	4008	3	US-08-307-896-5	Sequence 5, Appli
c 744	11.4	81.4	2601	3	US-10-232-286-3	Sequence 3, Appli	c 817	11.4	81.4	4008	3	US-08-726-214-3	Sequence 3, Appli
c 745	11.4	81.4	2601	4	US-10-334-717-3	Sequence 3, Appli	c 818	11.4	81.4	4008	7	PCT-US95-11808-5	Sequence 5, Appli
c 746	11.4	81.4	2601	7	PCT-US96-12860-3	Sequence 3, Appli	c 819	11.4	81.4	4060	2	US-08-308-949A-1	Sequence 1, Appli
c 747	11.4	81.4	2652	3	US-09-489-039A-2545	Sequence 2545, Ap	c 820	11.4	81.4	4062	3	US-09-873-737A-3	Sequence 3, Appli
c 748	11.4	81.4	2676	2	US-08-511-485-5	Sequence 5, Appli	c 821	11.4	81.4	4121	3	US-09-949-016-1777	Sequence 1777, Ap
c 749	11.4	81.4	2676	3	US-09-201-936-5	Sequence 5, Appli	c 822	11.4	81.4	4376	3	US-10-200-012-15	Sequence 15, Appl
c 750	11.4	81.4	2676	3	US-09-011-356-5	Sequence 5, Appli	c 823	11.4	81.4	4407	7	PCT-US93-05701-1	Sequence 1, Appli
c 751	11.4	81.4	2676	3	US-09-672-717-220	Sequence 220, App	c 824	11.4	81.4	4456	3	US-08-321-686B-1	Sequence 1, Appli
c 752	11.4	81.4	2676	3	US-09-201-932-5	Sequence 5, Appli	c 825	11.4	81.4	4522	7	PCT-US93-06251-22	Sequence 22, Appl
c 753	11.4	81.4	2676	4	US-09-654-743-5	Sequence 5, Appli	c 826	11.4	81.4	4529	3	US-09-949-016-14004	Sequence 14004, A

c 827	11.4	81.4	4545	3	US-09-897-425-53	Sequence 53, Appl	c 900	11.4	81.4	7194	4	US-10-428-826-76	Sequence 76, Appl
c 828	11.4	81.4	4546	3	US-09-897-425-50	Sequence 50, Appl	901	11.4	81.4	7243	3	US-09-949-016-5315	Sequence 5315, Ap
c 829	11.4	81.4	4628	3	US-09-949-016-5298	Sequence 5298, Ap	902	11.4	81.4	7410	3	US-09-973-278-748	Sequence 748, App
c 830	11.4	81.4	5100	2	US-08-164-292B-15	Sequence 15, Appl	903	11.4	81.4	7421	3	US-09-973-278-749	Sequence 749, App
c 831	11.4	81.4	5100	2	US-08-164-292B-17	Sequence 17, Appl	c 904	11.4	81.4	7453	3	US-09-949-016-16259	Sequence 16259, A
c 832	11.4	81.4	5100	2	US-08-164-292B-19	Sequence 19, Appl	c 905	11.4	81.4	7765	3	US-09-949-016-12771	Sequence 12771, A
c 833	11.4	81.4	5100	2	US-08-164-292B-21	Sequence 21, Appl	c 906	11.4	81.4	7765	3	US-09-949-016-13824	Sequence 13824, A
c 834	11.4	81.4	5100	2	US-08-164-292B-23	Sequence 23, Appl	c 907	11.4	81.4	7780	3	US-09-632-033B-2	Sequence 2, Appli
c 835	11.4	81.4	5100	2	US-08-164-292B-25	Sequence 25, Appl	c 908	11.4	81.4	7791	3	US-09-949-016-13900	Sequence 13900, A
c 836	11.4	81.4	5100	2	US-08-845-623-15	Sequence 15, Appl	c 909	11.4	81.4	7833	2	US-08-074-879-9	Sequence 9, Appli
c 837	11.4	81.4	5100	3	US-08-845-623-17	Sequence 17, Appl	c 910	11.4	81.4	7833	2	US-08-468-057A-9	Sequence 3804, Ap
c 838	11.4	81.4	5100	3	US-08-845-623-19	Sequence 19, Appl	c 911	11.4	81.4	7912	3	US-09-949-016-13804	Sequence 1, Appli
c 839	11.4	81.4	5100	3	US-08-845-623-21	Sequence 21, Appl	c 912	11.4	81.4	7940	3	US-09-632-033B-1	Sequence 17596, A
c 840	11.4	81.4	5100	3	US-08-845-623-23	Sequence 23, Appl	c 913	11.4	81.4	7948	3	US-09-949-016-17596	Sequence 97, Appl
c 841	11.4	81.4	5100	3	US-08-845-623-25	Sequence 25, Appl	c 914	11.4	81.4	9069	3	US-08-961-527-97	Sequence 13070, A
c 842	11.4	81.4	5100	3	US-08-815-927-15	Sequence 15, Appl	c 915	11.4	81.4	9132	3	US-09-949-016-13070	Sequence 22, Appl
c 843	11.4	81.4	5100	3	US-08-815-927-17	Sequence 17, Appl	c 916	11.4	81.4	9139	3	US-09-322-478-22	Sequence 22, Appl
c 844	11.4	81.4	5100	3	US-08-815-927-19	Sequence 19, Appl	c 917	11.4	81.4	9139	3	US-09-586-106D-22	Sequence 22, Appl
c 845	11.4	81.4	5100	3	US-08-815-927-21	Sequence 21, Appl	c 918	11.4	81.4	9139	3	US-10-799-870-22	Sequence 22, Appl
c 846	11.4	81.4	5100	3	US-08-815-927-23	Sequence 23, Appl	c 919	11.4	81.4	9299	3	US-08-458-434A-7	Sequence 7, Appli
c 847	11.4	81.4	5100	3	US-08-815-927-25	Sequence 25, Appl	c 920	11.4	81.4	9301	3	US-09-449-218D-18	Sequence 18, Appl
c 848	11.4	81.4	5100	3	US-09-103-330-15	Sequence 15, Appl	c 921	11.4	81.4	9301	3	US-09-668-529A-18	Sequence 18, Appl
c 849	11.4	81.4	5100	3	US-09-103-330-17	Sequence 17, Appl	c 922	11.4	81.4	9301	3	US-09-668-037A-18	Sequence 18, Appl
c 850	11.4	81.4	5100	3	US-09-103-330-19	Sequence 19, Appl	c 923	11.4	81.4	9301	3	US-09-668-021-18	Sequence 18, Appl
c 851	11.4	81.4	5100	3	US-09-103-330-21	Sequence 21, Appl	c 924	11.4	81.4	9556	3	US-09-902-540-982	Sequence 982, App
c 852	11.4	81.4	5100	3	US-09-103-330-23	Sequence 23, Appl	c 925	11.4	81.4	10091	3	US-09-058-483-34	Sequence 34, Appl
c 853	11.4	81.4	5100	3	US-09-103-330-25	Sequence 25, Appl	c 926	11.4	81.4	10597	3	US-09-949-016-13766	Sequence 13766, A
c 854	11.4	81.4	5100	3	US-09-435-242-15	Sequence 15, Appl	c 927	11.4	81.4	11225	10	5182210-9	Patent No. 5182210
c 855	11.4	81.4	5100	3	US-09-435-242-17	Sequence 17, Appl	c 928	11.4	81.4	11271	3	US-08-956-171E-11	Sequence 11, Appl
c 856	11.4	81.4	5100	3	US-09-435-242-19	Sequence 19, Appl	c 929	11.4	81.4	11271	3	US-08-781-986A-11	Sequence 11, Appl
c 857	11.4	81.4	5100	3	US-09-435-242-21	Sequence 21, Appl	c 930	11.4	81.4	11272	3	US-09-341-461-1	Sequence 2, Appli
c 858	11.4	81.4	5100	3	US-09-435-242-23	Sequence 23, Appl	c 931	11.4	81.4	11464	3	US-08-991-840A-2	Sequence 1, Appli
c 859	11.4	81.4	5100	3	US-09-435-242-25	Sequence 25, Appl	c 932	11.4	81.4	12626	3	US-09-949-002-685	Sequence 685, App
c 860	11.4	81.4	5100	5	US-10-046-938-15	Sequence 15, Appl	c 933	11.4	81.4	12752	2	US-08-459-146-1	Sequence 1, Appli
c 861	11.4	81.4	5100	5	US-10-046-938-17	Sequence 17, Appl	c 934	11.4	81.4	12752	2	US-08-459-065-1	Sequence 1, Appli
c 862	11.4	81.4	5100	5	US-10-046-938-19	Sequence 19, Appl	c 935	11.4	81.4	14094	3	US-09-949-016-14093	Sequence 14093, A
c 863	11.4	81.4	5100	5	US-10-046-938-21	Sequence 21, Appl	c 936	11.4	81.4	15393	3	US-09-453-702B-191	Sequence 191, App
c 864	11.4	81.4	5100	5	US-10-046-938-23	Sequence 23, Appl	c 937	11.4	81.4	15393	3	US-10-114-170-191	Sequence 191, App
c 865	11.4	81.4	5100	5	US-10-046-938-25	Sequence 25, Appl	c 938	11.4	81.4	15420	3	US-09-601-326-54	Sequence 54, Appl
c 866	11.4	81.4	5134	3	US-09-853-450-46	Sequence 46, Appl	c 939	11.4	81.4	15420	3	US-10-428-826-54	Sequence 54, Appl
c 867	11.4	81.4	5191	5	US-09-543-679A-2556	Sequence 2556, Ap	c 940	11.4	81.4	16207	3	US-09-949-016-16747	Sequence 16747, A
c 868	11.4	81.4	5307	3	US-10-028-056-2	Sequence 2, Appli	c 941	11.4	81.4	16236	3	US-09-949-016-16298	Sequence 16298, A
c 869	11.4	81.4	5418	3	US-09-893-525-38	Sequence 38, Appl	c 942	11.4	81.4	16344	3	US-09-949-016-16034	Sequence 16034, A
c 870	11.4	81.4	5521	3	US-08-975-762-48	Sequence 48, Appl	c 943	11.4	81.4	16716	3	US-09-949-016-17060	Sequence 17060, A
c 871	11.4	81.4	5521	3	US-09-295-028-48	Sequence 48, Appl	c 944	11.4	81.4	17488	3	US-09-949-016-15574	Sequence 15574, A
c 872	11.4	81.4	5521	3	US-09-106-582-48	Sequence 48, Appl	c 945	11.4	81.4	17930	3	US-09-949-016-11902	Sequence 11902, A
c 873	11.4	81.4	5521	3	US-09-159-469-48	Sequence 48, Appl	c 946	11.4	81.4	18048	3	US-09-949-016-12363	Sequence 12363, A
c 874	11.4	81.4	5521	3	US-09-693-542-48	Sequence 48, Appl	c 947	11.4	81.4	18049	3	US-09-949-016-15235	Sequence 15235, A
c 875	11.4	81.4	5535	2	US-08-089-758A-1	Sequence 1, Appli	c 948	11.4	81.4	18094	3	US-09-949-016-11719	Sequence 13179, A
c 876	11.4	81.4	5535	2	US-08-089-758A-4	Sequence 4, Appli	c 949	11.4	81.4	18351	3	US-09-949-016-16749	Sequence 16749, A
c 877	11.4	81.4	5535	2	US-08-421-754-1	Sequence 1, Appli	c 950	11.4	81.4	18492	3	US-09-949-016-17450	Sequence 17450, A
c 878	11.4	81.4	5535	2	US-08-421-754-4	Sequence 4, Appli	c 951	11.4	81.4	18494	3	US-09-949-016-15366	Sequence 15366, A
c 879	11.4	81.4	5535	2	US-08-421-791-1	Sequence 1, Appli	c 952	11.4	81.4	18534	3	US-09-949-016-13519	Sequence 13519, A
c 880	11.4	81.4	5535	2	US-08-421-791-4	Sequence 4, Appli	c 953	11.4	81.4	19167	3	US-09-949-016-12432	Sequence 12432, A
c 881	11.4	81.4	5734	3	US-09-976-594-862	Sequence 862, App	c 954	11.4	81.4	19302	3	US-09-902-540-1155	Sequence 1155, Ap
c 882	11.4	81.4	5795	3	US-09-949-016-13169	Sequence 13169, A	c 955	11.4	81.4	20026	3	US-09-949-016-13147	Sequence 13147, A
c 883	11.4	81.4	6063	2	US-08-195-744-4	Sequence 4, Appli	c 956	11.4	81.4	20182	3	US-09-949-016-13240	Sequence 13240, A
c 884	11.4	81.4	6063	2	US-08-788-279-4	Sequence 4, Appli	c 957	11.4	81.4	20221	3	US-09-949-016-15366	Sequence 15366, A
c 885	11.4	81.4	6184	3	US-09-590-968B-1	Sequence 1, Appli	c 958	11.4	81.4	20537	3	US-09-949-016-12887	Sequence 12887, A
c 886	11.4	81.4	6595	3	US-09-142-108C-9	Sequence 9, Appli	c 959	11.4	81.4	20538	3	US-09-949-016-17052	Sequence 17052, A
c 887	11.4	81.4	6610	3	US-09-949-016-14835	Sequence 14835, A	c 960	11.4	81.4	20599	3	US-09-949-016-14477	Sequence 14477, A
c 888	11.4	81.4	6611	3	US-09-949-016-12357	Sequence 12357, A	c 961	11.4	81.4	20599	3	US-09-949-016-14478	Sequence 14478, A
c 889	11.4	81.4	6669	3	US-09-212-971-5	Sequence 5, Appli	c 962	11.4	81.4	21360	3	US-09-949-016-12857	Sequence 12857, A
c 890	11.4	81.4	6669	3	US-08-800-929A-5	Sequence 5, Appli	c 963	11.4	81.4	21361	3	US-09-949-016-16245	Sequence 16245, A
c 891	11.4	81.4	6669	3	US-09-617-053A-5	Sequence 5, Appli	c 964	11.4	81.4	21513	3	US-09-949-016-16695	Sequence 16695, A
c 892	11.4	81.4	6669	3	US-09-672-717-230	Sequence 230, App	c 965	11.4	81.4	21513	3	US-09-949-016-16696	Sequence 16696, A
c 893	11.4	81.4	6830	2	US-08-822-445-1	Sequence 1, Appli	c 966	11.4	81.4	21513	3	US-09-949-016-16697	Sequence 16697, A
c 894	11.4	81.4	6830	3	US-09-396-540-1	Sequence 1, Appli	c 967	11.4	81.4	23193	3	US-09-949-016-17215	Sequence 17215, A
c 895	11.4	81.4	6975	3	US-09-949-016-15155	Sequence 15155, A	c 968	11.4	81.4	23568	3	US-09-949-016-14160	Sequence 14160, A
c 896	11.4	81.4	6995	3	US-09-531-266-1	Sequence 1, Appli	c 969	11.4	81.4	23679	3	US-09-949-016-15296	Sequence 15296, A
c 897	11.4	81.4	7070	3	US-09-949-016-12469	Sequence 12469, A	c 970	11.4	81.4	23672	3	US-09-949-016-12575	Sequence 12575, A
c 898	11.4	81.4	7070	3	US-09-949-016-15322	Sequence 15322, A	c 971	11.4	81.4	23672	3	US-09-949-016-12575	Sequence 12575, A
c 899	11.4	81.4	7194	3	US-09-601-326-76	Sequence 76, Appl	c 972	11.4	81.4	24405	3	US-09-949-016-19401	Sequence 12040, A

973 11.4 81.4 24405 3 US-09-949-016-17346 Sequence 17346, A
974 11.4 81.4 25356 3 US-09-976-594-750 Sequence 750, App
975 11.4 81.4 26076 3 US-09-949-002-831 Sequence 831, App
976 11.4 81.4 26116 3 US-09-949-016-16852 Sequence 16852, A
977 11.4 81.4 27284 3 US-09-949-016-15417 Sequence 15417, A
978 11.4 81.4 27377 3 US-09-816-248-18 Sequence 18, Appl
979 11.4 81.4 27617 3 US-09-949-016-17040 Sequence 17040, A
980 11.4 81.4 28203 3 US-09-949-016-16952 Sequence 16952, A
981 11.4 81.4 28203 3 US-09-949-016-16953 Sequence 16953, A
982 11.4 81.4 28203 3 US-09-949-016-16954 Sequence 16954, A
983 11.4 81.4 29430 3 US-09-544-398B-7 Sequence 7, Appli
984 11.4 81.4 29430 3 US-09-543-771B-7 Sequence 7, Appli
985 11.4 81.4 29935 3 US-09-949-016-11871 Sequence 11871, A
986 11.4 81.4 29936 3 US-09-949-016-14443 Sequence 14443, A
987 11.4 81.4 31440 3 US-09-949-016-12578 Sequence 12578, A
988 11.4 81.4 31444 3 US-09-949-016-16400 Sequence 16400, A
989 11.4 81.4 31545 3 US-09-949-016-17219 Sequence 17219, A
990 11.4 81.4 32669 3 US-09-949-016-17250 Sequence 17250, A
991 11.4 81.4 33248 3 US-09-596-002-24 Sequence 24, Appl
992 11.4 81.4 34446 3 US-09-103-330-35 Sequence 35, Appl
993 11.4 81.4 34446 3 US-09-871-212-1 Sequence 1, Appli
994 11.4 81.4 34531 3 US-09-949-016-14604 Sequence 14604, A
995 11.4 81.4 35081 2 US-08-752-760A-1 Sequence 1, Appli
996 11.4 81.4 35100 3 US-09-782-378A-26 Sequence 26, Appl
997 11.4 81.4 35337 3 US-09-949-016-17249 Sequence 17249, A
998 11.4 81.4 35524 3 US-08-923-137-1 Sequence 1, Appli
999 11.4 81.4 36519 3 US-08-923-137-2 Sequence 2, Appli
c1000 11.4 81.4 37319 3 US-09-949-016-13164 Sequence 13164, A

ALIGNMENTS

RESULT 1
US-09-248-796A-1942/c
; Sequence 1942, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1942
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1942

Query Match 100.0%; Score 14; DB 3; Length 774;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGCTTAC 14
|||
Db 761 GAAGGTGCTTAC 748

RESULT 2
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.

; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743.637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 14; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAGGTGCTTAC 14
|||
Db 1094 GAAGGTGCTTAC 1081
RESULT 3
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 14; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 4
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 14; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 1115 GAAGGTGTGCTTAC 1102

RESULT 5
US-09-620-412C-336/c
; Sequence 336, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-620-412C-336

Query Match 92.9%; Score 13; DB 3; Length 1758;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 1451 GAAGGTGTGCTTA 1439

RESULT 6
US-09-598-419-336/c
; Sequence 336, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-598-419-336

Query Match 92.9%; Score 13; DB 3; Length 1758;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 1451 GAAGGTGTGCTTA 1439

RESULT 7
US-08-309-341-1/c
; Sequence 1, Application US/08309341
; Patent No. 5594119
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5594119o No. 5594119disk of No. 5594119th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 14; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 4
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 14; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 1115 GAAGGTGTGCTTAC 1102

RESULT 5
US-09-620-412C-336/c
; Sequence 336, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-620-412C-336

Query Match 92.9%; Score 13; DB 3; Length 1758;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 1451 GAAGGTGTGCTTA 1439

RESULT 6
US-09-598-419-336/c
; Sequence 336, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-598-419-336

Query Match 92.9%; Score 13; DB 3; Length 1758;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 1451 GAAGGTGTGCTTA 1439

RESULT 7
US-08-309-341-1/c
; Sequence 1, Application US/08309341
; Patent No. 5594119
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5594119o No. 5594119disk of No. 5594119th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/309,341
/ FILING DATE: 16-SEP-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lowney, Karen A.
/ REGISTRATION NUMBER: 31,274
/ REFERENCE/DOCKET NUMBER: 4247.000-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 867 0123
/ TELEFAX: 212 867 0298
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2068 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ ORIGINAL SOURCE:
/ ORGANISM: Aspergillus niger
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 572..632
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: Join (571..633)
/ US-08-309-341-1

Query Match          92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AAGGTGTGCTTAC 14
Db      583 AAGGTGTGCTTAC 571

RESULT 8
US-08-608-267-1/c
/ Sequence 1, Application US/08608267
/ Patent No. 5688663
/ GENERAL INFORMATION:
/ APPLICANT: Yaver, Debbie Sue
/ APPLICANT: Thompson, Sheryl Ann
/ TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 5688663o No. 5688663disk of No. 5688663th America, Inc.
/ STREET: 405 Lexington Avenue, Suite 6400
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10174-6401
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/608,267
/ FILING DATE: 28-FEB-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/309,341
/ FILING DATE: 20-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lowney, Karen A.
/ REGISTRATION NUMBER: 31,274
/ REFERENCE/DOCKET NUMBER: 4247.000-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 867 0123
/ TELEFAX: 212 867 0298
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2068 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ ORIGINAL SOURCE:
/ ORGANISM: Aspergillus niger
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 572..632
/ TELEFAX: 212 867 0298
/ INFORMATION FOR SEQ ID NO: 1:
```

```
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2068 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ ORIGINAL SOURCE:
/ ORGANISM: Aspergillus niger
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 572..632
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: Join (571..633)
/ US-08-608-267-1

Query Match          92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AAGGTGTGCTTAC 14
Db      583 AAGGTGTGCTTAC 571

RESULT 9
US-08-608-452-1/c
/ Sequence 1, Application US/08608452
/ Patent No. 5693510
/ GENERAL INFORMATION:
/ APPLICANT: Yaver, Debbie Sue
/ APPLICANT: Thompson, Sheryl Ann
/ TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 5693510o No. 5693510disk of No. 5693510th America, Inc.
/ STREET: 405 Lexington Avenue, Suite 6400
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10174-6401
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/608,452
/ FILING DATE: 28-FEB-1996
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/309,341
/ FILING DATE: 20-SEP-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lowney, Karen A.
/ REGISTRATION NUMBER: 31,274
/ REFERENCE/DOCKET NUMBER: 4247.000-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 867 0123
/ TELEFAX: 212 867 0298
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2068 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ ORIGINAL SOURCE:
/ ORGANISM: Aspergillus niger
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 572..632
/ TELEFAX: 212 867 0298
/ INFORMATION FOR SEQ ID NO: 1:
```



```
; NAME/KEY: CDS
; LOCATION: join (571..633)
US-08-608-452-1

Query Match          92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       583 AAGGTGTGCTTAC 571

RESULT 10
US-08-608-224-1/c
; Sequence 1, Application US/08608224
; Patent No. 5705376
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5705376 No. 5705376disk of No. 5705376ch America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/608,224
; FILING DATE: 28-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,341
; FILING DATE: 20-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; FILING DATE: 20-SEP-1994
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: intron
; LOCATION: 572..632
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (571..633)
US-08-608-224-1

Query Match          92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       583 AAGGTGTGCTTAC 571

RESULT 11
US-08-967-149-1/c
; Sequence 1, Application US/08967149
; Patent No. 5939305
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5939305 No. 5939305disk of No. 5939305th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,149
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,452
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 08/309,341
; FILING DATE: 20-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: intron
; LOCATION: 572..632
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (571..633)
US-08-967-149-1

Query Match          92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       583 AAGGTGTGCTTAC 571

RESULT 12
US-10-197-220-165/c
; Sequence 165, Application US/10197220
; Patent No. 6919187
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Guderian, Jeff
; APPLICANT: Skeiky, Yasir A. W.
```

; APPLICANT: Maisonneuve, Jean-Francois L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; FILE REFERENCE: 210121.515C3
; CURRENT APPLICATION NUMBER: US/10/197,220
; CURRENT FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 165
; LENGTH: 4191
; TYPE: DNA
; ORGANISM: Chlamydia
US-10-197-220-165

Query Match 92.9%; Score 13; DB 3; Length 4191;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
|||||

Db 1925 GAAGGTGTGCTTA 1913
|||||

RESULT 13
US-09-556-877-174/c
; Sequence 174, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probat, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556, 877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 174
; LENGTH: 5265
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-174

Query Match 92.9%; Score 13; DB 3; Length 5265;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
|||||

Db 2003 GAAGGTGTGCTTA 1991
|||||

RESULT 14
US-09-620-412C-174/c
; Sequence 174, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 174
; LENGTH: 5265
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-174

Query Match 92.9%; Score 13; DB 3; Length 5265;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
|||||

Db 2003 GAAGGTGTGCTTA 1991
|||||

RESULT 15
US-09-598-419-174/c
; Sequence 174, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 174
; LENGTH: 5265
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-174

Query Match 92.9%; Score 13; DB 3; Length 5265;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
|||||

Db 2003 GAAGGTGTGCTTA 1991
|||||

RESULT 16
US-08-961-527-104/c
; Sequence 104, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 104:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 6735 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-08-961-527-104

Query Match          92.9%; Score 13; DB 3; Length 6735;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       5983 AAGGTGTGCTTAC 5971

RESULT 17
US-09-949-016-11759/c
; Sequence 11759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11759
;   LENGTH: 15164
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11759

Query Match          92.9%; Score 13; DB 3; Length 15164;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       13446 AAGGTGTGCTTAC 13434

RESULT 18
US-09-949-016-15664/c
; Sequence 15664, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15664
;   LENGTH: 15165
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15664

Query Match          92.9%; Score 13; DB 3; Length 15165;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       13446 AAGGTGTGCTTAC 13434

RESULT 19
US-09-949-016-13632
; Sequence 13632, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13632
;   LENGTH: 300402
;   TYPE: DNA
;   ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(300402)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13632

Query Match          92.9%; Score 13; DB 3; Length 300402;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       108237 AAGGTGTGCTTAC 108249

RESULT 20
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
;   LENGTH: 767677
;   TYPE: DNA
;   ORGANISM: Human
; FEATURE:
```



```
RESULT 25
US-09-198-452A-4479/c
; Sequence 4479, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffaia, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4479
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4479

Query Match      88.6%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGCTTAC 14
Db      18 GAAGGTGCTTAC 5

RESULT 26
US-10-131-827-258/c
; Sequence 258, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-258

Query Match      88.6%; Score 12.4; DB 3; Length 50;
Best Local Similarity 92.9%; Pred. No. 5.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGCTTAC 14
Db      19 GAAGGGTCTTAC 6

RESULT 27
US-10-131-831-258/c
; Sequence 258, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
```

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-258

Query Match      88.6%; Score 12.4; DB 5; Length 50;
Best Local Similarity 92.9%; Pred. No. 5.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGCTTAC 14
Db      19 GAAGGGTCTTAC 6

RESULT 28
US-09-583-110-1470
; Sequence 1470, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1470
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1470

Query Match      88.6%; Score 12.4; DB 3; Length 399;
Best Local Similarity 92.9%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGCTTAC 14
Db      328 GAAGGTGCTTAC 341

RESULT 29
US-09-605-703B-1409/c
; Sequence 1409, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
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; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1409
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(385)
; OTHER INFORMATION: RXN03032
US-09-605-703B-1409

Query Match      88.6%; Score 12.4; DB 4; Length 408;
Best Local Similarity 92.9%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      82 GATGGTGTGCTTAC 69

RESULT 30
US-09-605-703B-1413/c
; Sequence 1413, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1413
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(385)
; OTHER INFORMATION: FRXA00063
US-09-605-703B-1413

Query Match      88.6%; Score 12.4; DB 4; Length 408;
Best Local Similarity 92.9%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      82 GATGGTGTGCTTAC 69

RESULT 31
US-09-107-433-1001
; Sequence 1001, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
; THERAPEUTICS
```

```
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1001:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...414
; SEQUENCE DESCRIPTION: SEQ ID NO: 1001:
US-09-107-433-1001

Query Match      88.6%; Score 12.4; DB 3; Length 414;
Best Local Similarity 92.9%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      343 GAAGTTTGTCTTAC 356

RESULT 32
US-09-270-767-7793/c
; Sequence 7793, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7793
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7793

Query Match      88.6%; Score 12.4; DB 3; Length 489;
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Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 306 GATGGTGTGCTTAC 293

RESULT 33
US-09-270-767-23075/c
; Sequence 23075, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23075
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23075

Query Match 88.6%; Score 12.4; DB 3; Length 489;
Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 306 GATGGTGTGCTTAC 293

RESULT 34
US-09-949-016-26439/c
; Sequence 26439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26439
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26439

Query Match 88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 126 GAAGGTGTGCTTAC 113

RESULT 35
US-09-949-016-29854
; Sequence 29854, Application US/09949016
; Patent No. 6812339
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```
GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29854
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-29854

Query Match 88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 454 GAAGGTGTGCTTAC 467

RESULT 36
US-09-949-016-29855
; Sequence 29855, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29855
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-29855

Query Match 88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 32 GAAGGTGTGCTTAC 45

RESULT 37
US-09-949-016-52622/c
; Sequence 52622, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
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; SEQ ID NO 66349
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66349

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 59 GAAGGTGTGCTAC 46

RESULT 42
US-09-949-016-94388/c
; Sequence 94388, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94388
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94388

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 126 GAAGGTGTGCTTC 113

RESULT 43
US-09-949-016-105464
; Sequence 105464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105464
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105464

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 232 GAAGGTGTCTTAC 245

RESULT 44
US-09-949-016-105465
; Sequence 105465, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105465
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105465

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 232 GAAGGTGTCTTAC 245

RESULT 45
US-09-949-016-105466
; Sequence 105466, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105466
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105466

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 204 GAAGGTGTGCTTAC 217

RESULT 46

US-09-949-016-188180
; Sequence 188180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188180
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-188180

Query Match 88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 470 GAAGGTGTGCTTAC 483

RESULT 47

US-09-533-559-4801/c
; Sequence 4801, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849, 200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4801
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(649)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-4801

Query Match 88.6%; Score 12.4; DB 3; Length 649;
Best Local Similarity 92.9%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 155 GAAGGTGTGCTTAC 142

RESULT 48

US-09-533-559-5196
; Sequence 5196, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849, 200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5196
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(676)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-5196

Query Match 88.6%; Score 12.4; DB 3; Length 676;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 532 GTAGGTGTGCTTAC 545

RESULT 49

US-09-605-703B-1411/c
; Sequence 1411, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1411
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(660)
; OTHER INFORMATION: RXN03034
US-09-605-703B-1411

Query Match 88.6%; Score 12.4; DB 4; Length 683;
Best Local Similarity 92.9%; Pred. NO. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: May 31, 2006, 21:24:25
Job time : 138 secs

QY 1 GAAGGTGTCCTTAC 14
Db 357 GATGGTGTGCTTAC 344

RESULT 50

US-09-297-648-2528/c
; Sequence 2528, Application US/09297648
; Patent No. 6964868
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassan, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, William Lee
; APPLICANT: Stache-Crain, Birjit
; TITLE OF INVENTION: Products II
; FILE REFERENCE: 2300-1481
; CURRENT APPLICATION NUMBER: US/09/297,648
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,666
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,515
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 5252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2528
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(734)
; OTHER INFORMATION: n = A,T,C or G
US-09-297-648-2528

Query Match 88.6%; Score 12.4; DB 4; Length 734;
Best Local Similarity 92.9%; Pred. NO. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTCCTTAC 14
Db 709 GAAGGTGTCCTTAC 696

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:37:46 ; Search time 1470 Seconds
(without alignments)
117.025 Million cell updates/sec

Title: US-09-865-579A-19

Perfect score: 14

Sequence: 1 gaaggtgcttac 14

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Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA Main:*

1: /EMC Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /EMC Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
3: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
4: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
5: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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7: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
8: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
9: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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11: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
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15: /EMC Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
16: /EMC Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	14	100.0	14	3	US-09-865-579A-17	Sequence 17, Appl
2	14	100.0	14	3	US-09-865-579A-19	Sequence 19, Appl
C 3	14	100.0	22	10	US-10-735-357-44	Sequence 44, Appl
	4	100.0	22	10	US-10-735-357-75	Sequence 75, Appl
C 5	14	100.0	22	10	US-10-995-051-16	Sequence 16, Appl
C 6	14	100.0	281	10	US-10-995-051-14	Sequence 14, Appl
C 7	14	100.0	560	10	US-10-478-633A-151	Sequence 151, Appl
8	14	100.0	738	6	US-10-027-632-152712	Sequence 152712, Appl
9	14	100.0	738	6	US-10-027-632-152713	Sequence 152713, Appl
10	14	100.0	738	7	US-10-027-632-152712	Sequence 152712, Appl
11	14	100.0	738	7	US-10-027-632-152713	Sequence 152713, Appl
C 12	14	100.0	1502	8	US-10-425-114-2665	Sequence 2665, Appl
C 13	14	100.0	1502	9	US-10-425-115-102549	Sequence 102549, Appl
C 14	14	100.0	1957	9	US-10-479-674-82	Sequence 82, Appl
C 15	14	100.0	2007	3	US-09-452-599-169	Sequence 169, Appl
C 16	14	100.0	2007	7	US-10-121-120-169	Sequence 169, Appl
C 17	14	100.0	2007	9	US-10-479-674-78	Sequence 78, Appl

C 18	14	100.0	2007	9	US-10-479-674-90	Sequence 90, Appl
C 19	14	100.0	2007	9	US-10-479-674-91	Sequence 91, Appl
C 20	14	100.0	2007	9	US-10-121-120-169	Sequence 169, Appl
C 21	14	100.0	2015	8	US-10-320-797-1231	Sequence 1231, Appl
C 22	14	100.0	2028	8	US-10-724-972A-3141	Sequence 3141, Appl
C 23	14	100.0	4015	8	US-10-320-797-231	Sequence 231, Appl
C 24	13	92.9	25	9	US-10-719-900-225680	Sequence 225680, Appl
C 25	13	92.9	25	13	US-11-036-317-858913	Sequence 858913, Appl
C 26	13	92.9	25	13	US-11-036-317-863503	Sequence 863503, Appl
C 27	13	92.9	25	13	US-11-036-317-888398	Sequence 888398, Appl
C 28	13	92.9	25	13	US-11-036-317-958076	Sequence 958076, Appl
C 29	13	92.9	201	9	US-10-741-601-18514	Sequence 18514, Appl
C 30	13	92.9	201	9	US-10-741-600-50241	Sequence 50241, Appl
C 31	13	92.9	301	10	US-10-450-763-29551	Sequence 29551, Appl
C 32	13	92.9	335	8	US-10-424-599-6873	Sequence 6873, Appl
C 33	13	92.9	339	3	US-09-732-627A-1859	Sequence 1859, Appl
C 34	13	92.9	346	8	US-10-424-599-129096	Sequence 129096, Appl
C 35	13	92.9	418	4	US-09-925-065A-201193	Sequence 201193, Appl
C 36	13	92.9	418	5	US-09-925-065A-201193	Sequence 201193, Appl
C 37	13	92.9	426	4	US-09-925-065A-201194	Sequence 201194, Appl
C 38	13	92.9	426	5	US-09-925-065A-201194	Sequence 201194, Appl
C 39	13	92.9	427	12	US-10-301-480-289751	Sequence 289751, Appl
C 40	13	92.9	427	12	US-10-301-480-903160	Sequence 903160, Appl
C 41	13	92.9	443	4	US-09-925-065A-158432	Sequence 158432, Appl
C 42	13	92.9	443	5	US-09-925-065A-158432	Sequence 158432, Appl
C 43	13	92.9	459	8	US-10-437-963-95228	Sequence 95228, Appl
C 44	13	92.9	467	8	US-10-437-963-95228	Sequence 95228, Appl
C 45	13	92.9	468	4	US-09-925-065A-282736	Sequence 282736, Appl
C 46	13	92.9	468	4	US-09-925-065A-515582	Sequence 515582, Appl
C 47	13	92.9	468	5	US-09-925-065A-282736	Sequence 282736, Appl
C 48	13	92.9	468	5	US-09-925-065A-515582	Sequence 515582, Appl
C 49	13	92.9	474	12	US-10-301-480-359684	Sequence 359684, Appl
C 50	13	92.9	474	12	US-10-301-480-973093	Sequence 973093, Appl
C 51	13	92.9	483	9	US-10-425-115-166834	Sequence 166834, Appl
C 52	13	92.9	489	8	US-10-424-599-45528	Sequence 45528, Appl
C 53	13	92.9	501	4	US-09-925-065A-820200	Sequence 820200, Appl
C 54	13	92.9	501	5	US-09-925-065A-820200	Sequence 820200, Appl
C 55	13	92.9	508	7	US-10-029-386-1053	Sequence 1053, Appl
C 56	13	92.9	532	4	US-09-925-065A-139524	Sequence 139524, Appl
C 57	13	92.9	532	5	US-09-925-065A-139524	Sequence 139524, Appl
C 58	13	92.9	534	12	US-10-301-480-234597	Sequence 234597, Appl
C 59	13	92.9	534	12	US-10-301-480-848006	Sequence 848006, Appl
C 60	13	92.9	554	4	US-09-925-065A-261271	Sequence 261271, Appl
C 61	13	92.9	554	4	US-09-925-065A-261272	Sequence 261272, Appl
C 62	13	92.9	554	5	US-09-925-065A-261271	Sequence 261271, Appl
C 63	13	92.9	554	5	US-09-925-065A-261272	Sequence 261272, Appl
C 64	13	92.9	557	12	US-10-301-480-63509	Sequence 63509, Appl
C 65	13	92.9	557	12	US-10-301-480-63510	Sequence 63510, Appl
C 66	13	92.9	557	12	US-10-301-480-676918	Sequence 676918, Appl
C 67	13	92.9	557	12	US-10-301-480-676919	Sequence 676919, Appl
C 68	13	92.9	559	4	US-09-925-065A-267727	Sequence 267727, Appl
C 69	13	92.9	559	4	US-09-925-065A-488017	Sequence 488017, Appl
C 70	13	92.9	559	5	US-09-925-065A-267727	Sequence 267727, Appl
C 71	13	92.9	559	5	US-09-925-065A-488017	Sequence 488017, Appl
C 72	13	92.9	560	12	US-10-301-480-345488	Sequence 345488, Appl
C 73	13	92.9	560	12	US-10-301-480-958897	Sequence 958897, Appl
C 74	13	92.9	562	4	US-09-925-065A-227495	Sequence 227495, Appl
C 75	13	92.9	562	4	US-09-925-065A-227496	Sequence 227496, Appl
C 76	13	92.9	562	4	US-09-925-065A-227497	Sequence 227497, Appl
C 77	13	92.9	562	4	US-09-925-065A-227498	Sequence 227498, Appl
C 78	13	92.9	562	4	US-09-925-065A-790018	Sequence 790018, Appl
C 79	13	92.9	562	5	US-09-925-065A-227495	Sequence 227495, Appl
C 80	13	92.9	562	5	US-09-925-065A-227496	Sequence 227496, Appl
C 81	13	92.9	562	5	US-09-925-065A-227497	Sequence 227497, Appl
C 82	13	92.9	562	5	US-09-925-065A-227498	Sequence 227498, Appl
C 83	13	92.9	562	5	US-09-925-065A-790018	Sequence 790018, Appl
C 84	13	92.9	563	12	US-10-301-480-311682	Sequence 311682, Appl
C 85	13	92.9	563	12	US-10-301-480-311683	Sequence 311683, Appl
C 86	13	92.9	563	12	US-10-301-480-311684	Sequence 311684, Appl
C 87	13	92.9	563	12	US-10-301-480-311685	Sequence 311685, Appl
C 88	13	92.9	563	12	US-10-301-480-945091	Sequence 925091, Appl
C 89	13	92.9	563	12	US-10-301-480-945092	Sequence 925092, Appl
C 90	13	92.9	563	12	US-10-301-480-945093	Sequence 925093, Appl

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c 92	13	92.9	570	4	US-09-925-065A-811812	Sequence 811812,	165	13	92.9	1455	8	US-10-424-599-26067	Sequence 26067, A
c 93	13	92.9	570	4	US-09-925-065A-811812	Sequence 811812,	166	13	92.9	1455	8	US-10-425-114-10120	Sequence 10120, A
c 94	13	92.9	570	4	US-09-925-065A-811812	Sequence 811812,	167	13	92.9	1529	8	US-10-425-114-9676	Sequence 9676, Ap
c 95	13	92.9	570	5	US-09-925-065A-811812	Sequence 811812,	168	13	92.9	1529	8	US-09-841-132-336	Sequence 336, App
c 96	13	92.9	572	6	US-10-027-632-215572	Sequence 215572,	c 169	13	92.9	1758	9	US-10-872-155-336	Sequence 336, App
c 97	13	92.9	572	6	US-10-027-632-215573	Sequence 215573,	c 170	13	92.9	1821	8	US-10-705-716A-9	Sequence 9, Appl
c 98	13	92.9	572	7	US-10-027-632-215573	Sequence 215573,	171	13	92.9	1828	4	US-09-925-065A-699036	Sequence 699036,
c 99	13	92.9	572	7	US-10-027-632-215573	Sequence 215573,	172	13	92.9	1828	4	US-09-925-065A-699037	Sequence 699037,
c 100	13	92.9	573	4	US-09-925-065A-439654	Sequence 439654,	173	13	92.9	1828	4	US-09-925-065A-699038	Sequence 699038,
c 101	13	92.9	573	5	US-09-925-065A-439654	Sequence 439654,	174	13	92.9	1828	4	US-09-925-065A-699039	Sequence 699039,
c 102	13	92.9	574	12	US-10-301-480-500711	Sequence 500711,	175	13	92.9	1828	5	US-09-925-065A-699036	Sequence 699036,
c 103	13	92.9	574	12	US-10-301-480-1114120	Sequence 1114120,	176	13	92.9	1828	5	US-09-925-065A-699037	Sequence 699037,
c 104	13	92.9	575	6	US-10-027-632-108219	Sequence 108219,	177	13	92.9	1828	5	US-09-925-065A-699038	Sequence 699038,
c 105	13	92.9	575	7	US-10-027-632-108219	Sequence 108219,	178	13	92.9	1828	5	US-09-925-065A-699039	Sequence 699039,
c 106	13	92.9	576	12	US-10-301-480-215833	Sequence 215833,	c 179	13	92.9	1934	9	US-10-424-599-40697	Sequence 40697, A
c 107	13	92.9	576	12	US-10-301-480-829242	Sequence 829242,	c 180	13	92.9	1934	9	US-10-739-930-3656	Sequence 3656, A
c 108	13	92.9	577	4	US-09-925-065A-117031	Sequence 117031,	c 181	13	92.9	1977	8	US-10-425-114-8687	Sequence 8687, Ap
c 109	13	92.9	577	4	US-09-925-065A-117031	Sequence 117031,	182	13	92.9	1982	4	US-09-925-065A-177	Sequence 177, App
c 110	13	92.9	577	5	US-09-925-065A-117031	Sequence 117031,	183	13	92.9	1982	4	US-09-925-065A-177	Sequence 177, App
c 111	13	92.9	577	5	US-09-925-065A-117031	Sequence 117031,	c 184	13	92.9	1988	8	US-10-705-716A-7	Sequence 7, Appl
c 112	13	92.9	584	12	US-10-301-480-215834	Sequence 215834,	c 185	13	92.9	1994	16	US-11-096-568A-34080	Sequence 34080, A
c 113	13	92.9	584	12	US-10-301-480-829243	Sequence 829243,	c 186	13	92.9	1999	8	US-10-437-963-16019	Sequence 16019, A
c 114	13	92.9	587	4	US-09-925-065A-261269	Sequence 261269,	c 187	13	92.9	2063	8	US-10-424-599-11396	Sequence 11396, A
c 115	13	92.9	587	5	US-09-925-065A-261269	Sequence 261269,	c 188	13	92.9	2433	10	US-10-750-185-32670	Sequence 32670, A
c 116	13	92.9	588	12	US-10-301-480-339584	Sequence 339584,	c 189	13	92.9	2433	10	US-10-424-599-26056	Sequence 26056, A
c 117	13	92.9	588	12	US-10-301-480-952993	Sequence 952993,	c 190	13	92.9	2522	8	US-10-424-599-26056	Sequence 26056, A
c 118	13	92.9	591	4	US-09-925-065A-599652	Sequence 599652,	c 191	13	92.9	2660	10	US-10-469-204-7	Sequence 204-7
c 119	13	92.9	591	4	US-09-925-065A-599653	Sequence 599653,	c 192	13	92.9	2826	10	US-10-450-763-13292	Sequence 13292, A
c 120	13	92.9	591	5	US-09-925-065A-599652	Sequence 599652,	193	13	92.9	2826	10	US-10-450-763-14921	Sequence 14921, A
c 121	13	92.9	591	5	US-09-925-065A-599653	Sequence 599653,	194	13	92.9	2827	10	US-10-450-763-5461	Sequence 5461, Ap
c 122	13	92.9	594	4	US-09-925-065A-156571	Sequence 156571,	c 195	13	92.9	3966	8	US-10-437-963-54861	Sequence 54861, A
c 123	13	92.9	594	5	US-09-925-065A-156571	Sequence 156571,	c 196	13	92.9	4191	10	US-10-197-220-165	Sequence 165, App
c 124	13	92.9	594	12	US-10-301-480-249787	Sequence 249787,	c 197	13	92.9	4191	10	US-11-099-468-165	Sequence 165, App
c 125	13	92.9	594	12	US-10-301-480-863196	Sequence 863196,	c 198	13	92.9	5253	3	US-09-841-132-421	Sequence 421, App
c 126	13	92.9	596	12	US-10-301-480-8467	Sequence 8467,	c 199	13	92.9	5253	3	US-09-841-132-421	Sequence 421, App
c 127	13	92.9	596	12	US-10-301-480-621876	Sequence 621876,	c 200	13	92.9	5253	3	US-10-872-155-421	Sequence 421, App
c 128	13	92.9	630	4	US-09-925-065A-831434	Sequence 831434,	c 201	13	92.9	5256	8	US-10-467-534-46	Sequence 46, Appl
c 129	13	92.9	630	5	US-09-925-065A-831434	Sequence 831434,	c 202	13	92.9	5256	10	US-10-498-327-116	Sequence 116, App
c 130	13	92.9	633	4	US-09-925-065A-839505	Sequence 839505,	c 203	13	92.9	5256	15	US-11-103-957-46	Sequence 46, Appl
c 131	13	92.9	633	5	US-09-925-065A-839505	Sequence 839505,	c 204	13	92.9	5256	15	US-09-841-132-174	Sequence 174, App
c 132	13	92.9	668	12	US-10-301-480-101414	Sequence 101414,	c 205	13	92.9	5265	3	US-10-872-155-174	Sequence 174, App
c 133	13	92.9	668	12	US-10-301-480-714823	Sequence 714823,	c 206	13	92.9	5265	3	US-08-961-527-104	Sequence 104, App
c 134	13	92.9	676	8	US-10-767-701-7451	Sequence 7451, Ap	c 207	13	92.9	6735	2	US-10-158-844-104	Sequence 104, App
c 135	13	92.9	705	6	US-10-437-963-16677	Sequence 16677, A	c 208	13	92.9	6735	7	US-10-074-024-739	Sequence 739, App
c 136	13	92.9	739	6	US-10-027-632-17138	Sequence 17138, A	c 209	13	92.9	11853	7	US-10-270-333-43	Sequence 43, Appl
c 137	13	92.9	739	6	US-10-027-632-17138	Sequence 17138, A	c 210	13	92.9	14111	6	US-11-097-143-12829	Sequence 12829, A
c 138	13	92.9	739	7	US-10-027-632-139762	Sequence 139762,	c 211	13	92.9	14111	9	US-10-741-600-17699	Sequence 17699, A
c 139	13	92.9	743	4	US-09-925-065A-937054	Sequence 937054,	c 212	13	92.9	50353	9	US-10-995-561-13305	Sequence 13305, A
c 140	13	92.9	743	5	US-09-925-065A-937054	Sequence 937054,	c 213	13	92.9	50353	10	US-10-322-281-395	Sequence 395, App
c 141	13	92.9	743	5	US-09-925-065A-937054	Sequence 937054,	c 214	13	92.9	50353	8	US-10-052-482-193	Sequence 193, App
c 142	13	92.9	756	6	US-10-027-632-261233	Sequence 261233,	c 215	13	92.9	72732	8	US-10-322-281-341	Sequence 341, App
c 143	13	92.9	756	7	US-10-027-632-261233	Sequence 261233,	c 216	13	92.9	91278	8	US-10-322-281-341	Sequence 49, Appl
c 144	13	92.9	756	12	US-10-301-480-96047	Sequence 96047, A	c 217	13	92.9	93483	7	US-10-034-650-49	Sequence 53, Appl
c 145	13	92.9	756	12	US-10-301-480-709456	Sequence 709456,	c 218	13	92.9	102145	9	US-10-331-053-53	Sequence 1987, Ap
c 146	13	92.9	765	4	US-09-925-065A-942176	Sequence 942176,	c 219	13	92.9	134841	6	US-10-087-192-1987	Sequence 1987, Ap
c 147	13	92.9	765	5	US-09-925-065A-942176	Sequence 942176,	c 220	13	92.9	157044	6	US-10-087-192-1987	Sequence 1987, Ap
c 148	13	92.9	776	4	US-09-925-065A-922002	Sequence 922002,	c 221	13	92.9	410846	10	US-10-481-613-1	Sequence 1, Appl
c 149	13	92.9	776	5	US-09-925-065A-922002	Sequence 922002,	c 222	13	92.9	561515	8	US-10-741-601-5682	Sequence 5682, Ap
c 150	13	92.9	995	12	US-10-301-480-566094	Sequence 566094,	c 223	13	92.9	561515	9	US-10-741-601-17730	Sequence 17730, A
c 151	13	92.9	995	12	US-10-301-480-1179503	Sequence 1179503,	c 224	13	92.9	653458	10	US-10-461-862-4	Sequence 4, Appl
c 152	13	92.9	1072	8	US-10-425-114-10222	Sequence 10222, A	c 225	13	92.9	2162593	9	US-10-472-928-4979	Sequence 4979, Ap
c 153	13	92.9	1085	8	US-10-425-114-10222	Sequence 10222, A	c 226	12.6	90.0	243	9	US-10-333-872A-183	Sequence 183, App
c 154	13	92.9	1219	12	US-10-301-480-40530	Sequence 40530, A	c 227	12.6	90.0	360	12	US-10-301-480-15871	Sequence 15871, A
c 155	13	92.9	1219	12	US-10-301-480-40531	Sequence 40531, A	c 228	12.6	90.0	360	12	US-10-301-480-629280	Sequence 629280
c 156	13	92.9	1219	12	US-10-301-480-653939	Sequence 653939,	c 229	12.6	90.0	424	12	US-10-301-480-15870	Sequence 15870, A
c 157	13	92.9	1219	12	US-10-301-480-653940	Sequence 653940,	c 230	12.6	90.0	424	12	US-10-301-480-629279	Sequence 629279, A
c 158	13	92.9	1234	6	US-10-027-632-123700	Sequence 123700,	c 231	12.6	90.0	426	4	US-09-925-065A-201192	Sequence 201192,
c 159	13	92.9	1234	6	US-10-027-632-123700	Sequence 123700,	c 232	12.6	90.0	426	5	US-09-925-065A-201192	Sequence 201192,
c 160	13	92.9	1234	7	US-10-027-632-123700	Sequence 123700,	c 233	12.6	90.0	427	5	US-10-301-480-289750	Sequence 289750,
c 161	13	92.9	1242	10	US-10-750-185-30919	Sequence 30919, A	c 234	12.6	90.0	427	12	US-10-301-480-903159	Sequence 903159,
c 162	13	92.9	1242	10	US-10-750-185-30919	Sequence 30919, A	c 235	12.6	90.0	573	4	US-09-925-065A-439653	Sequence 439653,
c 163	13	92.9	1242	10	US-10-750-185-30919	Sequence 30919, A	c 236	12.6	90.0	573	5	US-09-925-065A-439653	Sequence 439653,

C 237	12.6	90.0	574	12	US-10-301-480-500710	Sequence 500710,	C 310	12.4	88.6	376	12	US-10-301-480-1073045	Sequence 1073045,
C 238	12.6	90.0	574	12	US-10-301-480-111419	Sequence 111419,	C 311	12.4	88.6	381	3	US-09-732-627A-1613	Sequence 1613, App
C 239	12.4	88.6	19	14	US-11-083-784-251000	Sequence 251000,	C 312	12.4	88.6	383	10	US-10-779-543-10524	Sequence 10524, A
C 240	12.4	88.6	19	14	US-11-083-784-465057	Sequence 465057,	C 313	12.4	88.6	386	9	US-10-357-930-46046	Sequence 46046, A
C 241	12.4	88.6	19	14	US-11-083-784-1546339	Sequence 1546339,	C 314	12.4	88.6	386	9	US-10-357-930-47176	Sequence 47176, A
C 242	12.4	88.6	19	15	US-11-101-244-251000	Sequence 251000,	C 315	12.4	88.6	392	9	US-10-425-115-150312	Sequence 150312, A
C 243	12.4	88.6	19	15	US-11-101-244-465057	Sequence 465057,	C 316	12.4	88.6	393	9	US-10-425-115-94251	Sequence 94251, A
C 244	12.4	88.6	19	15	US-11-101-244-1546339	Sequence 1546339,	C 317	12.4	88.6	394	10	US-10-779-543-16180	Sequence 16180, A
C 245	12.4	88.6	20	7	US-10-289-762-1978	Sequence 1978, App	C 318	12.4	88.6	396	9	US-10-472-928-263	Sequence 263, App
C 246	12.4	88.6	20	7	US-10-289-762-4479	Sequence 4479, App	C 319	12.4	88.6	398	9	US-10-425-115-177673	Sequence 177673, A
C 247	12.4	88.6	21	11	US-10-310-914A-212681	Sequence 212681,	C 320	12.4	88.6	399	3	US-09-815-243-9114	Sequence 9114, App
C 248	12.4	88.6	24	11	US-10-310-914A-212682	Sequence 212682,	C 321	12.4	88.6	399	3	US-09-815-243-9472	Sequence 9472, App
C 249	12.4	88.6	25	8	US-10-719-956-50987	Sequence 50987, A	C 322	12.4	88.6	399	8	US-10-282-122A-37553	Sequence 37553, A
C 250	12.4	88.6	25	8	US-10-719-956-256067	Sequence 256067,	C 323	12.4	88.6	403	9	US-10-425-115-169458	Sequence 169458, A
C 251	12.4	88.6	25	8	US-10-719-956-311710	Sequence 311710,	C 324	12.4	88.6	404	9	US-10-767-793-1647	Sequence 1647, App
C 252	12.4	88.6	25	8	US-10-719-956-389564	Sequence 389564,	C 325	12.4	88.6	408	3	US-09-783-590-3620	Sequence 3620, App
C 253	12.4	88.6	25	8	US-10-719-956-450851	Sequence 450851,	C 326	12.4	88.6	414	7	US-10-007-926A-369	Sequence 369, App
C 254	12.4	88.6	25	8	US-10-719-956-573001	Sequence 573001,	C 327	12.4	88.6	414	8	US-10-474-776-445	Sequence 445, App
C 255	12.4	88.6	25	8	US-10-719-956-680581	Sequence 680581,	C 328	12.4	88.6	414	10	US-10-617-320-1001	Sequence 1001, App
C 256	12.4	88.6	25	9	US-10-719-900-272853	Sequence 272853,	C 329	12.4	88.6	418	3	US-09-960-352-12566	Sequence 12566, A
C 257	12.4	88.6	25	9	US-10-719-900-431528	Sequence 431528,	C 330	12.4	88.6	433	6	US-10-027-632-183308	Sequence 183308, A
C 258	12.4	88.6	25	9	US-10-719-900-440516	Sequence 440516,	C 331	12.4	88.6	433	7	US-10-027-632-183308	Sequence 183308, A
C 259	12.4	88.6	25	9	US-10-719-900-644391	Sequence 644391,	C 332	12.4	88.6	436	12	US-10-301-480-272348	Sequence 272348, A
C 260	12.4	88.6	25	9	US-10-719-900-898049	Sequence 898049,	C 333	12.4	88.6	436	12	US-10-301-480-885757	Sequence 885757, A
C 261	12.4	88.6	25	11	US-10-933-982-81140	Sequence 81140, A	C 334	12.4	88.6	440	4	US-09-925-065A-181686	Sequence 181686, A
C 262	12.4	88.6	25	13	US-11-036-317-7709	Sequence 7709, App	C 335	12.4	88.6	440	5	US-09-925-065A-181686	Sequence 181686, A
C 263	12.4	88.6	25	13	US-11-036-317-8293	Sequence 8293, App	C 336	12.4	88.6	442	3	US-09-764-891-658	Sequence 658, App
C 264	12.4	88.6	25	13	US-11-036-317-29791	Sequence 29791, A	C 337	12.4	88.6	459	3	US-09-864-761-102	Sequence 102, App
C 265	12.4	88.6	25	13	US-11-036-317-444094	Sequence 444094,	C 338	12.4	88.6	466	9	US-10-437-963-28842	Sequence 28842, A
C 266	12.4	88.6	25	13	US-11-036-317-634816	Sequence 634816,	C 339	12.4	88.6	466	9	US-10-674-124A-7709	Sequence 7709, App
C 267	12.4	88.6	25	15	US-11-121-849-147659	Sequence 147659,	C 340	12.4	88.6	471	4	US-09-925-065A-354629	Sequence 354629, A
C 268	12.4	88.6	25	15	US-11-121-849-333005	Sequence 333005,	C 341	12.4	88.6	471	4	US-09-925-065A-526333	Sequence 526333, A
C 269	12.4	88.6	25	15	US-11-121-849-469995	Sequence 469995,	C 342	12.4	88.6	471	5	US-09-925-065A-354629	Sequence 354629, A
C 270	12.4	88.6	33	9	US-10-784-880-1661	Sequence 1661, App	C 343	12.4	88.6	471	5	US-09-925-065A-526333	Sequence 526333, A
C 271	12.4	88.6	50	7	US-10-131-827-258	Sequence 258, App	C 344	12.4	88.6	474	8	US-10-437-963-18033	Sequence 18033, A
C 272	12.4	88.6	50	16	US-11-175-859-32523	Sequence 32523, A	C 345	12.4	88.6	481	12	US-10-301-480-426189	Sequence 426189, A
C 273	12.4	88.6	200	16	US-11-098-686-2600	Sequence 2600, App	C 346	12.4	88.6	481	12	US-10-301-480-1039598	Sequence 1039598, A
C 274	12.4	88.6	201	9	US-10-437-963-85281	Sequence 85281, A	C 347	12.4	88.6	484	9	US-10-425-115-64611	Sequence 64611, A
C 275	12.4	88.6	201	9	US-10-719-993-28792	Sequence 28792, A	C 348	12.4	88.6	489	3	US-09-918-995-31255	Sequence 31255, A
C 276	12.4	88.6	201	10	US-10-995-561-29917	Sequence 29917, A	C 349	12.4	88.6	490	4	US-09-925-065A-369726	Sequence 369726, A
C 277	12.4	88.6	201	10	US-10-995-561-57506	Sequence 57506, A	C 350	12.4	88.6	490	4	US-09-925-065A-369727	Sequence 369727, A
C 278	12.4	88.6	201	10	US-10-995-561-57529	Sequence 57529, A	C 351	12.4	88.6	490	4	US-09-925-065A-611327	Sequence 611327, A
C 279	12.4	88.6	201	10	US-10-995-561-68777	Sequence 68777, A	C 352	12.4	88.6	490	5	US-09-925-065A-369726	Sequence 369726, A
C 280	12.4	88.6	201	15	US-11-124-368A-7150	Sequence 7150, App	C 353	12.4	88.6	490	5	US-09-925-065A-369727	Sequence 369727, A
C 281	12.4	88.6	201	16	US-11-124-368A-11403	Sequence 11403, A	C 354	12.4	88.6	490	8	US-09-925-065A-611327	Sequence 611327, A
C 282	12.4	88.6	201	16	US-11-124-367A-10054	Sequence 10054, A	C 355	12.4	88.6	490	8	US-10-767-701-22110	Sequence 22110, A
C 283	12.4	88.6	201	16	US-11-124-367A-12387	Sequence 12387, A	C 356	12.4	88.6	491	4	US-09-925-065A-844615	Sequence 844615, A
C 284	12.4	88.6	201	16	US-11-124-367A-12388	Sequence 12388, A	C 357	12.4	88.6	491	5	US-09-925-065A-844615	Sequence 844615, A
C 285	12.4	88.6	201	16	US-11-124-367A-21774	Sequence 21774, A	C 358	12.4	88.6	491	12	US-10-301-480-439811	Sequence 439811, A
C 286	12.4	88.6	233	3	US-09-983-963-5426	Sequence 5426, App	C 359	12.4	88.6	491	12	US-10-301-480-439812	Sequence 439812, A
C 287	12.4	88.6	233	9	US-10-357-930-16429	Sequence 16429, A	C 360	12.4	88.6	491	12	US-10-301-480-1053220	Sequence 1053220, A
C 288	12.4	88.6	241	12	US-10-301-480-398388	Sequence 398388, A	C 361	12.4	88.6	491	12	US-10-301-480-1053221	Sequence 1053221, A
C 289	12.4	88.6	241	12	US-10-301-480-1011797	Sequence 1011797, A	C 362	12.4	88.6	492	9	US-10-425-115-1411	Sequence 1411, App
C 290	12.4	88.6	244	4	US-09-925-065A-323943	Sequence 323943, A	C 363	12.4	88.6	493	4	US-09-925-065A-539179	Sequence 539179, A
C 291	12.4	88.6	244	5	US-09-925-065A-323943	Sequence 323943, A	C 364	12.4	88.6	493	4	US-09-925-065A-539180	Sequence 539180, A
C 292	12.4	88.6	254	8	US-10-424-599-109218	Sequence 109218, A	C 365	12.4	88.6	493	5	US-09-925-065A-539179	Sequence 539179, A
C 293	12.4	88.6	275	9	US-10-357-930-16220	Sequence 16220, A	C 366	12.4	88.6	493	5	US-09-925-065A-539180	Sequence 539180, A
C 294	12.4	88.6	282	9	US-10-357-930-17353	Sequence 17353, A	C 367	12.4	88.6	493	8	US-10-424-599-82326	Sequence 82326, A
C 295	12.4	88.6	313	3	US-09-764-891-7077	Sequence 7077, App	C 368	12.4	88.6	495	3	US-09-918-995-30723	Sequence 30723, A
C 296	12.4	88.6	320	7	US-10-007-926A-279	Sequence 279, App	C 369	12.4	88.6	496	4	US-09-925-065A-532142	Sequence 532142, A
C 297	12.4	88.6	321	9	US-10-425-115-17912	Sequence 17912, A	C 370	12.4	88.6	496	4	US-09-925-065A-532143	Sequence 532143, A
C 298	12.4	88.6	329	9	US-10-357-930-46255	Sequence 46255, A	C 371	12.4	88.6	496	5	US-09-925-065A-532142	Sequence 532142, A
C 299	12.4	88.6	333	7	US-10-369-493-45351	Sequence 45351, A	C 372	12.4	88.6	496	5	US-09-925-065A-532143	Sequence 532143, A
C 300	12.4	88.6	350	8	US-10-424-599-86263	Sequence 86263, A	C 373	12.4	88.6	497	9	US-10-425-115-181434	Sequence 181434, A
C 301	12.4	88.6	353	7	US-10-029-386-17106	Sequence 17106, A	C 374	12.4	88.6	500	3	US-09-783-590-3621	Sequence 3621, App
C 302	12.4	88.6	357	4	US-09-925-065A-391409	Sequence 391409, A	C 375	12.4	88.6	501	4	US-09-925-065A-164891	Sequence 164891, A
C 303	12.4	88.6	357	5	US-09-925-065A-391409	Sequence 391409, A	C 376	12.4	88.6	501	5	US-09-925-065A-164891	Sequence 164891, A
C 304	12.4	88.6	364	8	US-10-437-963-90151	Sequence 90151, A	C 377	12.4	88.6	506	12	US-10-301-480-386350	Sequence 386350, A
C 305	12.4	88.6	371	4	US-09-925-065A-616000	Sequence 616000, A	C 378	12.4	88.6	506	12	US-10-301-480-999759	Sequence 999759, A
C 306	12.4	88.6	371	5	US-09-925-065A-616000	Sequence 616000, A	C 379	12.4	88.6	507	4	US-09-925-065A-310923	Sequence 310923, A
C 307	12.4	88.6	372	3	US-10-156-761-1243	Sequence 1243, App	C 380	12.4	88.6	507	5	US-09-925-065A-310923	Sequence 310923, A
C 308	12.4	88.6	376	3	US-10-918-995-4426	Sequence 4426, App	C 381	12.4	88.6	507	10	US-10-779-543-16141	Sequence 16141, A
C 309	12.4	88.6	376	12	US-10-301-480-459636	Sequence 459636, A	C 382	12.4	88.6	508	12	US-10-301-480-457226	Sequence 457226, A

383	12.4	88.6	508	12	US-10-301-480-870635	Sequence 870635,	456	12.4	88.6	554	12	US-10-301-480-468168	Sequence 468168,
384	12.4	88.6	510	4	US-09-925-065A-164892	Sequence 164892,	457	12.4	88.6	554	12	US-10-301-480-1081577	Sequence 1081577,
385	12.4	88.6	510	5	US-09-925-065A-164892	Sequence 164892,	458	12.4	88.6	555	4	US-09-925-065A-798660	Sequence 798660,
386	12.4	88.6	510	16	US-11-079-463-3936	Sequence 3936, Ap	459	12.4	88.6	555	4	US-09-925-065A-945710	Sequence 945710,
387	12.4	88.6	515	9	US-10-425-115-152409	Sequence 152409,	460	12.4	88.6	555	5	US-09-925-065A-798660	Sequence 798660,
388	12.4	88.6	517	12	US-10-301-480-9	Sequence 9,	461	12.4	88.6	555	5	US-09-925-065A-945710	Sequence 945710,
389	12.4	88.6	517	12	US-10-301-480-257227	Sequence 257227,	c 462	12.4	88.6	556	4	US-09-925-065A-18150	Sequence 18150, A
390	12.4	88.6	517	12	US-10-301-480-613418	Sequence 613418,	c 463	12.4	88.6	556	5	US-09-925-065A-18150	Sequence 18150, A
391	12.4	88.6	517	12	US-10-301-480-870636	Sequence 870636,	c 464	12.4	88.6	556	12	US-10-301-480-119387	Sequence 119387,
392	12.4	88.6	518	6	US-10-027-632-98340	Sequence 98340, A	c 465	12.4	88.6	556	12	US-10-301-480-732796	Sequence 732796,
393	12.4	88.6	518	7	US-10-027-632-98340	Sequence 98340, A	c 466	12.4	88.6	557	4	US-09-925-065A-435867	Sequence 435867,
394	12.4	88.6	521	6	US-10-198-846-8321	Sequence 8321, Ap	467	12.4	88.6	557	4	US-09-925-065A-435868	Sequence 435868,
395	12.4	88.6	521	7	US-10-029-386-4001	Sequence 4001, Ap	468	12.4	88.6	557	4	US-09-925-065A-435869	Sequence 435869,
396	12.4	88.6	524	9	US-10-425-115-7448	Sequence 7448, Ap	469	12.4	88.6	557	5	US-09-925-065A-435867	Sequence 435867,
397	12.4	88.6	526	4	US-09-925-065A-332775	Sequence 332775,	470	12.4	88.6	557	5	US-09-925-065A-435868	Sequence 435868,
398	12.4	88.6	526	5	US-09-925-065A-332775	Sequence 332775,	471	12.4	88.6	557	5	US-09-925-065A-435869	Sequence 435869,
399	12.4	88.6	528	4	US-09-925-065A-15310	Sequence 15310, A	c 472	12.4	88.6	558	4	US-09-925-065A-615757	Sequence 615757,
400	12.4	88.6	528	4	US-09-925-065A-15311	Sequence 15311, A	c 473	12.4	88.6	558	5	US-09-925-065A-615757	Sequence 615757,
401	12.4	88.6	528	5	US-09-925-065A-15310	Sequence 15310, A	c 474	12.4	88.6	561	7	US-10-029-386-3404	Sequence 3404, Ap
402	12.4	88.6	528	5	US-09-925-065A-15311	Sequence 15311, A	c 475	12.4	88.6	562	4	US-09-925-065A-583934	Sequence 583934,
403	12.4	88.6	528	12	US-10-301-480-116547	Sequence 116547,	c 476	12.4	88.6	562	5	US-09-925-065A-583934	Sequence 583934,
404	12.4	88.6	528	12	US-10-301-480-116548	Sequence 116548,	c 477	12.4	88.6	564	4	US-09-925-065A-793338	Sequence 793338,
405	12.4	88.6	528	12	US-10-301-480-729956	Sequence 729956,	c 478	12.4	88.6	564	4	US-09-925-065A-793339	Sequence 793339,
406	12.4	88.6	528	12	US-10-301-480-729957	Sequence 729957,	c 479	12.4	88.6	564	4	US-09-925-065A-849688	Sequence 849688,
407	12.4	88.6	529	4	US-09-925-065A-563678	Sequence 563678,	c 480	12.4	88.6	564	4	US-09-925-065A-849689	Sequence 849689,
408	12.4	88.6	529	4	US-09-925-065A-563679	Sequence 563679,	c 481	12.4	88.6	564	5	US-09-925-065A-793338	Sequence 793338,
409	12.4	88.6	529	5	US-09-925-065A-563678	Sequence 563678,	c 482	12.4	88.6	564	5	US-09-925-065A-793339	Sequence 793339,
410	12.4	88.6	529	5	US-09-925-065A-563679	Sequence 563679,	c 483	12.4	88.6	564	5	US-09-925-065A-849688	Sequence 849688,
411	12.4	88.6	530	6	US-10-027-632-51449	Sequence 51449, A	c 484	12.4	88.6	566	4	US-09-925-065A-534050	Sequence 534050,
412	12.4	88.6	530	6	US-10-027-632-51449	Sequence 51449, A	c 485	12.4	88.6	566	4	US-09-925-065A-534050	Sequence 534050,
413	12.4	88.6	530	7	US-10-027-632-321291	Sequence 321291,	c 486	12.4	88.6	566	5	US-09-925-065A-534050	Sequence 534050,
414	12.4	88.6	530	7	US-10-027-632-321291	Sequence 321291,	c 487	12.4	88.6	567	4	US-09-925-065A-349379	Sequence 349379,
415	12.4	88.6	530	7	US-10-027-632-321291	Sequence 321291,	c 488	12.4	88.6	567	5	US-09-925-065A-349379	Sequence 349379,
416	12.4	88.6	530	7	US-10-027-632-321291	Sequence 321291,	c 489	12.4	88.6	569	4	US-09-925-065A-339327	Sequence 339327,
417	12.4	88.6	530	9	US-10-425-115-62072	Sequence 62072, A	c 490	12.4	88.6	569	5	US-09-925-065A-339327	Sequence 339327,
418	12.4	88.6	534	12	US-10-301-480-406421	Sequence 406421,	c 491	12.4	88.6	571	4	US-09-925-065A-401004	Sequence 401004,
419	12.4	88.6	534	12	US-10-301-480-1019830	Sequence 1019830,	c 492	12.4	88.6	571	4	US-09-925-065A-443186	Sequence 443186,
420	12.4	88.6	535	7	US-10-029-386-1254	Sequence 1254, Ap	c 493	12.4	88.6	571	5	US-09-925-065A-401004	Sequence 401004,
421	12.4	88.6	538	4	US-09-925-065A-188125	Sequence 188125,	c 494	12.4	88.6	571	5	US-09-925-065A-443186	Sequence 443186,
422	12.4	88.6	538	5	US-09-925-065A-188125	Sequence 188125,	c 495	12.4	88.6	572	6	US-10-027-632-184982	Sequence 184982,
423	12.4	88.6	539	4	US-09-925-065A-46112	Sequence 46112, A	c 496	12.4	88.6	572	6	US-10-027-632-184982	Sequence 184982,
424	12.4	88.6	539	4	US-09-925-065A-46112	Sequence 46112, A	c 497	12.4	88.6	574	4	US-09-925-065A-343030	Sequence 343030,
425	12.4	88.6	539	4	US-09-925-065A-192185	Sequence 192185,	c 498	12.4	88.6	574	4	US-09-925-065A-343030	Sequence 343030,
426	12.4	88.6	539	5	US-09-925-065A-197443	Sequence 197443,	c 499	12.4	88.6	574	5	US-09-925-065A-343030	Sequence 343030,
427	12.4	88.6	539	5	US-09-925-065A-46112	Sequence 46112, A	c 500	12.4	88.6	574	5	US-09-925-065A-343030	Sequence 343030,
428	12.4	88.6	539	5	US-09-925-065A-192185	Sequence 192185,	c 501	12.4	88.6	574	9	US-10-425-115-90364	Sequence 90364, A
429	12.4	88.6	539	5	US-09-925-065A-197443	Sequence 197443,	c 502	12.4	88.6	576	12	US-10-301-480-214276	Sequence 214276,
430	12.4	88.6	539	12	US-10-301-480-147350	Sequence 147350,	c 503	12.4	88.6	576	12	US-10-301-480-827685	Sequence 827685,
431	12.4	88.6	542	8	US-10-301-480-760759	Sequence 760759,	c 504	12.4	88.6	577	4	US-09-925-065A-115297	Sequence 115297,
432	12.4	88.6	543	4	US-09-925-065A-770952	Sequence 770952,	c 505	12.4	88.6	577	4	US-09-925-065A-925093	Sequence 925093,
433	12.4	88.6	543	5	US-09-925-065A-770952	Sequence 770952,	c 506	12.4	88.6	577	5	US-09-925-065A-115297	Sequence 115297,
434	12.4	88.6	543	12	US-10-301-480-286389	Sequence 286389,	c 507	12.4	88.6	577	5	US-09-925-065A-925093	Sequence 925093,
435	12.4	88.6	543	12	US-10-301-480-899798	Sequence 899798,	c 508	12.4	88.6	577	5	US-10-027-632-284927	Sequence 284927,
436	12.4	88.6	544	12	US-10-301-480-281751	Sequence 281751,	c 509	12.4	88.6	577	7	US-10-027-632-284927	Sequence 284927,
437	12.4	88.6	544	12	US-10-301-480-895160	Sequence 895160,	c 510	12.4	88.6	580	12	US-10-301-480-366598	Sequence 366598,
438	12.4	88.6	548	4	US-09-925-065A-306500	Sequence 306500,	c 511	12.4	88.6	580	12	US-10-301-480-382404	Sequence 382404,
439	12.4	88.6	548	4	US-09-925-065A-306501	Sequence 306501,	c 512	12.4	88.6	580	12	US-10-301-480-382405	Sequence 382405,
440	12.4	88.6	548	4	US-09-925-065A-306502	Sequence 306502,	c 513	12.4	88.6	580	12	US-10-301-480-382406	Sequence 382406,
441	12.4	88.6	548	4	US-09-925-065A-306503	Sequence 306503,	c 514	12.4	88.6	580	12	US-10-301-480-980007	Sequence 980007,
442	12.4	88.6	548	5	US-09-925-065A-306500	Sequence 306500,	c 515	12.4	88.6	580	12	US-10-301-480-995813	Sequence 995813,
443	12.4	88.6	548	5	US-09-925-065A-306501	Sequence 306501,	c 516	12.4	88.6	580	12	US-10-301-480-995814	Sequence 995814,
444	12.4	88.6	548	5	US-09-925-065A-306502	Sequence 306502,	c 517	12.4	88.6	581	12	US-10-301-480-995815	Sequence 995815,
445	12.4	88.6	548	5	US-09-925-065A-306503	Sequence 306503,	c 518	12.4	88.6	581	4	US-09-925-065A-289696	Sequence 289696,
446	12.4	88.6	551	4	US-09-925-065A-470875	Sequence 470875,	c 519	12.4	88.6	581	5	US-09-925-065A-289696	Sequence 289696,
447	12.4	88.6	551	5	US-09-925-065A-470875	Sequence 470875,	c 520	12.4	88.6	581	12	US-10-301-480-415741	Sequence 415741,
448	12.4	88.6	553	4	US-09-925-065A-44794	Sequence 44794, A	c 521	12.4	88.6	581	12	US-10-301-480-415742	Sequence 415742,
449	12.4	88.6	553	4	US-09-925-065A-44795	Sequence 44795, A	c 522	12.4	88.6	581	12	US-10-301-480-1029150	Sequence 1029150,
450	12.4	88.6	553	5	US-09-925-065A-44794	Sequence 44794, A	c 523	12.4	88.6	581	12	US-10-301-480-1029151	Sequence 1029151,
451	12.4	88.6	553	5	US-09-925-065A-44795	Sequence 44795, A	c 524	12.4	88.6	585	4	US-09-925-065A-433545	Sequence 433545,
452	12.4	88.6	553	12	US-10-301-480-146032	Sequence 146032,	c 525	12.4	88.6	585	5	US-09-925-065A-433545	Sequence 433545,
453	12.4	88.6	553	12	US-10-301-480-146033	Sequence 146033,	c 526	12.4	88.6	585	4	US-09-925-065A-165655	Sequence 165655,
454	12.4	88.6	553	12	US-10-301-480-759441	Sequence 759441,	c 527	12.4	88.6	586	4	US-09-925-065A-165656	Sequence 165656,
455	12.4	88.6	553	12	US-10-301-480-759442	Sequence 759442,	c 528	12.4	88.6	586	5	US-09-925-065A-165655	Sequence 165655,

529	12.4	88.6	586	5	US-09-925-065A-165656	Sequence 165656,	C 602	12.4	88.6	611	4	US-09-925-065A-275028	Sequence 275028,
530	12.4	88.6	586	12	US-10-301-480-435015	Sequence 435015,	C 603	12.4	88.6	611	5	US-09-925-065A-275028	Sequence 275028,
531	12.4	88.6	586	12	US-10-301-480-1048424	Sequence 1048424,	C 604	12.4	88.6	611	6	US-10-027-632-234629	Sequence 234629,
532	12.4	88.6	587	12	US-10-301-480-503647	Sequence 503647,	C 605	12.4	88.6	611	7	US-10-027-632-234629	Sequence 234629,
533	12.4	88.6	587	12	US-10-301-480-1117056	Sequence 1117056,	C 606	12.4	88.6	612	12	US-10-301-480-201183	Sequence 201183,
534	12.4	88.6	591	4	US-09-925-065A-687811	Sequence 687811,	C 607	12.4	88.6	612	12	US-10-301-480-814592	Sequence 814592,
535	12.4	88.6	591	5	US-09-925-065A-687811	Sequence 687811,	C 608	12.4	88.6	613	4	US-09-925-065A-908266	Sequence 908266,
536	12.4	88.6	592	4	US-09-925-065A-98740	Sequence 98740, A	C 609	12.4	88.6	613	5	US-09-925-065A-908266	Sequence 908266,
537	12.4	88.6	592	5	US-09-925-065A-98740	Sequence 98740, A	C 610	12.4	88.6	613	6	US-10-027-632-89461	Sequence 89461, A
538	12.4	88.6	592	12	US-10-301-480-495836	Sequence 495836,	C 611	12.4	88.6	613	7	US-10-027-632-89461	Sequence 89461, A
539	12.4	88.6	593	12	US-10-301-480-1109245	Sequence 1109245,	C 612	12.4	88.6	613	12	US-10-301-480-255290	Sequence 255290,
540	12.4	88.6	593	4	US-09-925-065A-776566	Sequence 776566,	C 613	12.4	88.6	613	12	US-10-301-480-868699	Sequence 868699,
541	12.4	88.6	593	4	US-09-925-065A-780799	Sequence 780799,	C 614	12.4	88.6	614	8	US-10-767-701-30524	Sequence 30524, A
542	12.4	88.6	593	5	US-09-925-065A-776566	Sequence 776566,	C 615	12.4	88.6	616	4	US-09-925-065A-897394	Sequence 897394,
543	12.4	88.6	593	5	US-09-925-065A-780799	Sequence 780799,	C 616	12.4	88.6	616	5	US-09-925-065A-897394	Sequence 897394,
544	12.4	88.6	593	7	US-10-029-386-4842	Sequence 4842, Ap	C 617	12.4	88.6	618	12	US-10-301-480-352060	Sequence 352060,
545	12.4	88.6	593	12	US-10-301-480-8908	Sequence 8908, Ap	C 618	12.4	88.6	618	12	US-10-301-480-965469	Sequence 965469,
546	12.4	88.6	593	12	US-10-301-480-622317	Sequence 622317,	C 619	12.4	88.6	618	6	US-10-027-632-183865	Sequence 183865,
547	12.4	88.6	594	4	US-09-925-065A-364358	Sequence 364358,	C 620	12.4	88.6	618	7	US-10-027-632-183865	Sequence 183865,
548	12.4	88.6	594	4	US-09-925-065A-635362	Sequence 635362,	C 621	12.4	88.6	619	12	US-10-301-480-582353	Sequence 582353,
549	12.4	88.6	594	5	US-09-925-065A-364358	Sequence 364358,	C 622	12.4	88.6	620	4	US-09-925-065A-162753	Sequence 162753,
550	12.4	88.6	594	5	US-09-925-065A-635362	Sequence 635362,	C 623	12.4	88.6	620	5	US-09-925-065A-162753	Sequence 162753,
551	12.4	88.6	594	6	US-10-027-632-279643	Sequence 279643,	C 624	12.4	88.6	620	6	US-10-027-632-46756	Sequence 46756, A
552	12.4	88.6	594	6	US-10-027-632-279644	Sequence 279644,	C 625	12.4	88.6	620	6	US-10-027-632-46756	Sequence 46756, A
553	12.4	88.6	594	6	US-10-027-632-279645	Sequence 279645,	C 626	12.4	88.6	620	7	US-10-027-632-46756	Sequence 46756, A
554	12.4	88.6	594	7	US-10-027-632-279643	Sequence 279643,	C 627	12.4	88.6	621	4	US-09-925-065A-270421	Sequence 270421,
555	12.4	88.6	594	7	US-10-027-632-279644	Sequence 279644,	C 628	12.4	88.6	621	4	US-09-925-065A-270422	Sequence 270422,
556	12.4	88.6	594	7	US-10-027-632-279645	Sequence 279645,	C 629	12.4	88.6	621	4	US-09-925-065A-336752	Sequence 336752,
557	12.4	88.6	595	12	US-10-301-480-43877	Sequence 43877, A	C 630	12.4	88.6	621	4	US-09-925-065A-852246	Sequence 852246,
558	12.4	88.6	595	12	US-10-301-480-657286	Sequence 657286,	C 631	12.4	88.6	621	5	US-09-925-065A-853922	Sequence 853922,
559	12.4	88.6	597	4	US-09-925-065A-444199	Sequence 444199,	C 632	12.4	88.6	621	5	US-09-925-065A-270421	Sequence 270421,
560	12.4	88.6	597	4	US-09-925-065A-444200	Sequence 444200,	C 633	12.4	88.6	621	5	US-09-925-065A-270422	Sequence 270422,
561	12.4	88.6	597	5	US-09-925-065A-444199	Sequence 444199,	C 634	12.4	88.6	621	5	US-09-925-065A-336752	Sequence 336752,
562	12.4	88.6	597	5	US-09-925-065A-444200	Sequence 444200,	C 635	12.4	88.6	621	5	US-09-925-065A-852246	Sequence 852246,
563	12.4	88.6	597	12	US-10-301-480-257937	Sequence 257937,	C 636	12.4	88.6	621	5	US-09-925-065A-853922	Sequence 853922,
564	12.4	88.6	597	12	US-10-301-480-257938	Sequence 257938,	C 637	12.4	88.6	621	5	US-09-925-065A-853922	Sequence 853922,
565	12.4	88.6	597	12	US-10-301-480-871346	Sequence 871346,	C 638	12.4	88.6	621	5	US-10-301-480-75678	Sequence 75678, A
566	12.4	88.6	597	12	US-10-301-480-871347	Sequence 871347,	C 639	12.4	88.6	621	5	US-10-301-480-689087	Sequence 689087,
567	12.4	88.6	598	6	US-10-027-632-235461	Sequence 235461,	C 640	12.4	88.6	630	12	US-09-925-065A-702321	Sequence 702321,
568	12.4	88.6	598	7	US-10-027-632-235461	Sequence 235461,	C 641	12.4	88.6	631	5	US-09-925-065A-702321	Sequence 702321,
569	12.4	88.6	598	12	US-10-301-480-199523	Sequence 199523,	C 642	12.4	88.6	637	5	US-09-925-065A-677846	Sequence 677846,
570	12.4	88.6	598	12	US-10-301-480-812932	Sequence 812932,	C 643	12.4	88.6	637	5	US-09-925-065A-677846	Sequence 677846,
571	12.4	88.6	599	4	US-09-925-065A-429150	Sequence 429150,	C 644	12.4	88.6	638	4	US-09-925-065A-499965	Sequence 499965,
572	12.4	88.6	599	4	US-09-925-065A-429151	Sequence 429151,	C 645	12.4	88.6	638	5	US-09-925-065A-499965	Sequence 499965,
573	12.4	88.6	599	5	US-09-925-065A-429150	Sequence 429150,	C 646	12.4	88.6	647	3	US-09-764-891-6597	Sequence 6597, Ap
574	12.4	88.6	599	5	US-09-925-065A-429151	Sequence 429151,	C 647	12.4	88.6	649	9	US-10-653-047-4801	Sequence 4801, Ap
575	12.4	88.6	599	12	US-10-301-480-504474	Sequence 504474,	C 648	12.4	88.6	650	6	US-10-027-632-235592	Sequence 235592,
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577	12.4	88.6	600	10	US-10-972-079-4487	Sequence 4487, Ap	C 650	12.4	88.6	650	8	US-10-437-963-61472	Sequence 61472, A
578	12.4	88.6	600	10	US-10-972-079-26733	Sequence 26733, A	C 651	12.4	88.6	650	8	US-09-925-065A-695517	Sequence 695517,
579	12.4	88.6	600	10	US-10-972-079-75108	Sequence 75108, A	C 652	12.4	88.6	654	4	US-09-925-065A-695518	Sequence 695518,
580	12.4	88.6	600	16	US-11-136-527-6126	Sequence 6126, Ap	C 653	12.4	88.6	654	5	US-09-925-065A-695517	Sequence 695517,
581	12.4	88.6	601	7	US-10-027-632-267414	Sequence 267414,	C 654	12.4	88.6	654	5	US-09-925-065A-695518	Sequence 695518,
582	12.4	88.6	601	7	US-10-027-632-267414	Sequence 267414,	C 655	12.4	88.6	654	5	US-09-925-065A-695518	Sequence 695518,
583	12.4	88.6	602	12	US-10-301-480-347904	Sequence 347904,	C 656	12.4	88.6	667	8	US-09-925-065A-909013	Sequence 909013,
584	12.4	88.6	602	12	US-10-301-480-347905	Sequence 347905,	C 657	12.4	88.6	667	8	US-10-424-598-108031	Sequence 108031,
585	12.4	88.6	602	12	US-10-301-480-961313	Sequence 961313,	C 658	12.4	88.6	667	12	US-10-301-480-70676	Sequence 70676, A
586	12.4	88.6	602	12	US-10-301-480-961314	Sequence 961314,	C 659	12.4	88.6	667	12	US-10-301-480-684085	Sequence 684085,
587	12.4	88.6	603	8	US-10-021-323-13632	Sequence 13632, A	C 660	12.4	88.6	673	4	US-09-925-065A-573178	Sequence 573178,
588	12.4	88.6	603	9	US-10-357-930-50221	Sequence 50221, A	C 661	12.4	88.6	673	5	US-09-925-065A-573178	Sequence 573178,
589	12.4	88.6	604	4	US-09-925-065A-753926	Sequence 753926,	C 662	12.4	88.6	676	9	US-10-653-047-5196	Sequence 5196, Ap
590	12.4	88.6	604	5	US-09-925-065A-753926	Sequence 753926,	C 663	12.4	88.6	679	4	US-09-925-065A-92876	Sequence 92876, A
591	12.4	88.6	606	4	US-09-925-065A-100604	Sequence 100604,	C 664	12.4	88.6	679	5	US-09-925-065A-92876	Sequence 92876, A
592	12.4	88.6	606	5	US-09-925-065A-100604	Sequence 100604,	C 665	12.4	88.6	679	12	US-10-301-480-194118	Sequence 194118,
593	12.4	88.6	606	9	US-10-767-795-3677	Sequence 3677, Ap	C 666	12.4	88.6	679	12	US-10-027-632-227235	Sequence 807527,
594	12.4	88.6	606	12	US-10-301-480-492088	Sequence 492088,	C 667	12.4	88.6	689	7	US-10-027-632-227235	Sequence 227235,
595	12.4	88.6	606	12	US-10-301-480-492089	Sequence 492089,	C 668	12.4	88.6	689	7	US-10-027-632-227235	Sequence 227235,
596	12.4	88.6	606	12	US-10-301-480-504473	Sequence 504473,	C 669	12.4	88.6	689	3	US-09-814-353-16993	Sequence 16993, A
597	12.4	88.6	606	12	US-10-301-480-1105497	Sequence 1105497,	C 670	12.4	88.6	693	4	US-09-925-065A-947694	Sequence 947694,
598	12.4	88.6	606	12	US-10-301-480-1105498	Sequence 1105498,	C 671	12.4	88.6	693	5	US-09-925-065A-947694	Sequence 947694,
599	12.4	88.6	606	12	US-10-301-480-1117882	Sequence 1117882,	C 672	12.4	88.6	693	5	US-09-925-065A-947695	Sequence 947695,
600	12.4	88.6	610	4	US-09-925-065A-245070	Sequence 245070,	C 673	12.4	88.6	697	10	US-10-750-185-25465	Sequence 25465, A
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C 821	12.4	88.6	1451	10	US-10-287-436A-574	Sequence 574, App	894	12.4	88.6	2192	8	US-10-302-172-658	Sequence 658, App
C 822	12.4	88.6	1451	15	US-11-105-268-57	Sequence 57, App	895	12.4	88.6	2224	6	US-10-027-632-102238	Sequence 102238, App
C 823	12.4	88.6	1456	3	US-09-822-849A-159	Sequence 159, App	896	12.4	88.6	2224	7	US-10-027-632-102238	Sequence 102238, App
C 824	12.4	88.6	1465	4	US-09-925-065A-724783	Sequence 724783, App	C 897	12.4	88.6	2226	8	US-10-437-963-101510	Sequence 101510, App
C 825	12.4	88.6	1465	4	US-09-925-065A-724784	Sequence 724784, App	C 898	12.4	88.6	2231	8	US-10-437-963-101510	Sequence 101510, App
C 826	12.4	88.6	1465	4	US-09-925-065A-724785	Sequence 724785, App	C 899	12.4	88.6	2251	9	US-10-739-930-4634	Sequence 70909, App
C 827	12.4	88.6	1465	4	US-09-925-065A-724786	Sequence 724786, App	C 900	12.4	88.6	2251	9	US-09-925-065A-702883	Sequence 702883, App
C 828	12.4	88.6	1465	4	US-09-925-065A-724787	Sequence 724787, App	C 901	12.4	88.6	2259	4	US-09-925-065A-702884	Sequence 702884, App
C 829	12.4	88.6	1465	5	US-09-925-065A-724788	Sequence 724788, App	C 902	12.4	88.6	2259	5	US-09-925-065A-702884	Sequence 702884, App
C 830	12.4	88.6	1465	5	US-09-925-065A-724789	Sequence 724789, App	C 903	12.4	88.6	2259	5	US-09-925-065A-702884	Sequence 702884, App
C 831	12.4	88.6	1465	5	US-09-925-065A-724785	Sequence 724785, App	C 904	12.4	88.6	2279	6	US-10-425-115-43622	Sequence 43622, App
C 832	12.4	88.6	1465	5	US-09-925-065A-724786	Sequence 724786, App	C 905	12.4	88.6	2279	6	US-10-027-632-265879	Sequence 265879, App
C 833	12.4	88.6	1465	5	US-09-925-065A-724787	Sequence 724787, App	C 906	12.4	88.6	2324	12	US-10-027-632-265879	Sequence 265879, App
C 834	12.4	88.6	1473	7	US-09-738-626-1401	Sequence 1401, App	C 907	12.4	88.6	2324	12	US-10-301-480-100707	Sequence 100707, App
C 835	12.4	88.6	1506	7	US-10-120-988-301	Sequence 301, App	C 908	12.4	88.6	2324	12	US-10-301-480-714116	Sequence 714116, App
C 836	12.4	88.6	1560	13	US-11-097-143-3380	Sequence 3380, App	C 909	12.4	88.6	2409	9	US-10-781-014-721	Sequence 721, App
C 837	12.4	88.6	1663	10	US-10-750-185-57070	Sequence 57070, App	C 910	12.4	88.6	2479	8	US-10-424-599-101161	Sequence 101161, App
C 838	12.4	88.6	1663	10	US-10-750-623-57070	Sequence 57070, App	C 911	12.4	88.6	2523	7	US-10-369-493-45949	Sequence 45949, App
C 839	12.4	88.6	1671	9	US-10-739-930-5100	Sequence 5100, App	C 912	12.4	88.6	2566	16	US-11-096-568A-24711	Sequence 24711, App
C 840	12.4	88.6	1692	8	US-10-755-889-661	Sequence 661, App	C 913	12.4	88.6	2635	10	US-10-450-763-25039	Sequence 25039, App
C 841	12.4	88.6	1710	8	US-10-494-672-339	Sequence 13623, App	C 914	12.4	88.6	2683	13	US-11-097-143-40027	Sequence 40027, App
C 842	12.4	88.6	1729	9	US-10-494-672-339	Sequence 339, App	C 915	12.4	88.6	2721	10	US-10-764-420-2368	Sequence 2368, App
C 843	12.4	88.6	1749	7	US-09-925-065A-49840	Sequence 49840, App	C 916	12.4	88.6	2725	6	US-10-087-192-188	Sequence 188, App
C 844	12.4	88.6	1771	4	US-09-925-065A-49840	Sequence 49840, App	C 917	12.4	88.6	2765	3	US-09-946-290-19	Sequence 19, App
C 845	12.4	88.6	1771	4	US-09-925-065A-49841	Sequence 49841, App	C 918	12.4	88.6	2811	9	US-10-425-114-27734	Sequence 27734, App
C 846	12.4	88.6	1771	4	US-09-925-065A-49842	Sequence 49842, App	C 919	12.4	88.6	2889	8	US-10-425-115-35763	Sequence 35763, App
C 847	12.4	88.6	1771	5	US-09-925-065A-49842	Sequence 49842, App	C 920	12.4	88.6	3008	13	US-11-097-143-19417	Sequence 19417, App
C 848	12.4	88.6	1771	5	US-09-925-065A-49841	Sequence 49841, App	C 921	12.4	88.6	3014	8	US-10-425-114-31589	Sequence 31589, App
C 849	12.4	88.6	1771	5	US-09-925-065A-49842	Sequence 49842, App	C 922	12.4	88.6	3050	9	US-10-473-126-29	Sequence 29, App
C 850	12.4	88.6	1771	12	US-10-301-480-151078	Sequence 151078, App	C 923	12.4	88.6	3083	13	US-11-097-143-27445	Sequence 27445, App
C 851	12.4	88.6	1771	12	US-10-301-480-151079	Sequence 151079, App	C 924	12.4	88.6	3125	13	US-11-097-143-40030	Sequence 40030, App
C 852	12.4	88.6	1771	12	US-10-301-480-151080	Sequence 151080, App	C 925	12.4	88.6	3129	3	US-09-938-842A-2286	Sequence 2286, App
C 853	12.4	88.6	1771	12	US-10-301-480-764487	Sequence 764487, App	C 926	12.4	88.6	3129	3	US-09-938-842A-2286	Sequence 2286, App
C 854	12.4	88.6	1771	12	US-10-301-480-764488	Sequence 764488, App	C 927	12.4	88.6	3130	4	US-09-925-065A-720418	Sequence 720418, App
C 855	12.4	88.6	1771	12	US-10-301-480-764489	Sequence 764489, App	C 928	12.4	88.6	3130	5	US-09-925-065A-720419	Sequence 720419, App
C 856	12.4	88.6	1788	8	US-10-282-122A-8691	Sequence 8691, App	C 929	12.4	88.6	3130	5	US-09-925-065A-720418	Sequence 720418, App
C 857	12.4	88.6	1799	8	US-10-702-395-32	Sequence 32, App	C 930	12.4	88.6	3130	5	US-09-925-065A-720419	Sequence 720419, App
C 858	12.4	88.6	1830	10	US-10-750-185-42726	Sequence 42726, App	C 931	12.4	88.6	3131	8	US-10-437-963-101511	Sequence 101511, App
C 859	12.4	88.6	1830	10	US-10-750-623-42726	Sequence 42726, App	C 932	12.4	88.6	3162	13	US-11-097-143-610	Sequence 610, App
C 860	12.4	88.6	1836	3	US-09-864-761-16939	Sequence 16939, App	C 933	12.4	88.6	3209	10	US-10-450-763-28925	Sequence 28925, App
C 861	12.4	88.6	1863	7	US-10-369-493-34422	Sequence 34422, App	C 934	12.4	88.6	3237	16	US-11-096-568A-33584	Sequence 33584, App
C 862	12.4	88.6	1893	9	US-10-425-115-60177	Sequence 60177, App	C 935	12.4	88.6	3256	4	US-09-925-065A-688254	Sequence 688254, App
C 863	12.4	88.6	1907	9	US-10-767-795-1645	Sequence 1645, App	C 936	12.4	88.6	3256	5	US-09-925-065A-688254	Sequence 688254, App
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C 865	12.4	88.6	1932	8	US-10-437-963-101509	Sequence 101509, App	C 938	12.4	88.6	3290	8	US-10-437-963-3759	Sequence 3759, App
C 866	12.4	88.6	1942	10	US-10-750-185-31647	Sequence 31647, App	C 939	12.4	88.6	3304	8	US-10-437-963-24077	Sequence 24077, App
C 867	12.4	88.6	1942	10	US-10-750-623-31647	Sequence 31647, App	C 940	12.4	88.6	3328	13	US-11-097-143-2422	Sequence 2422, App
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C 869	12.4	88.6	1975	10	US-10-750-185-44865	Sequence 44865, App	C 942	12.4	88.6	3378	16	US-11-036-196-1495	Sequence 1495, App
C 870	12.4	88.6	2031	6	US-10-750-623-44865	Sequence 44865, App	C 943	12.4	88.6	3378	16	US-10-437-963-88454	Sequence 88454, App
C 871	12.4	88.6	2031	6	US-10-750-623-258085	Sequence 258085, App	C 944	12.4	88.6	3398	8	US-10-437-963-88454	Sequence 88454, App
C 872	12.4	88.6	2031	7	US-10-027-632-258085	Sequence 258085, App	C 945	12.4	88.6	3621	9	US-10-425-115-144351	Sequence 144351, App
C 873	12.4	88.6	2031	12	US-10-301-480-92889	Sequence 92889, App	C 946	12.4	88.6	3621	13	US-11-097-143-3379	Sequence 3379, App
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C 879	12.4	88.6	2054	6	US-10-027-632-99944	Sequence 99944, App	C 952	12.4	88.6	3972	8	US-10-275-026A-37	Sequence 37, App
C 880	12.4	88.6	2054	6	US-10-027-632-99945	Sequence 99945, App	C 953	12.4	88.6	3979	7	US-10-191-997-96	Sequence 96, App
C 881	12.4	88.6	2054	6	US-10-027-632-99946	Sequence 99946, App	C 954	12.4	88.6	4083	7	US-10-258-746-1	Sequence 1, App
C 882	12.4	88.6	2054	7	US-10-027-632-97584	Sequence 97584, App	C 955	12.4	88.6	4083	7	US-10-258-746-1	Sequence 1, App
C 883	12.4	88.6	2054	7	US-10-027-632-99944	Sequence 99944, App	C 956	12.4	88.6	4095	16	US-11-136-527-2030	Sequence 2030, App
C 884	12.4	88.6	2054	7	US-10-027-632-99945	Sequence 99945, App	C 957	12.4	88.6	4237	3	US-09-978-522-4	Sequence 4, App
C 885	12.4	88.6	2054	7	US-10-027-632-99946	Sequence 99946, App	C 958	12.4	88.6	4371	10	US-10-450-763-7102	Sequence 7102, App
C 886	12.4	88.6	2054	8	US-10-027-632-99946	Sequence 99946, App	C 959	12.4	88.6	4371	10	US-10-450-763-24505	Sequence 24505, App
C 887	12.4	88.6	2054	11	US-10-932-182A-82278	Sequence 82278, App	C 960	12.4	88.6	4550	3	US-10-450-763-26898	Sequence 26898, App
C 888	12.4	88.6	2082	8	US-10-424-599-91349	Sequence 91349, App	C 961	12.4	88.6	4550	3	US-09-853-526-182	Sequence 182, App
C 889	12.4	88.6	2083	10	US-10-887-553A-883	Sequence 883, App	C 962	12.4	88.6	4683	3	US-09-070-927A-193	Sequence 193, App
C 890	12.4	88.6	2133	3	US-09-738-626-590	Sequence 590, App	C 963	12.4	88.6	4683	3	US-09-978-522-2	Sequence 2, App
C 891	12.4	88.6	2147	10	US-10-750-185-32983	Sequence 32983, App	C 964	12.4	88.6	4754	13	US-11-097-143-7390	Sequence 7390, App
C 892	12.4	88.6	2147	10	US-10-750-623-32983	Sequence 32983, App	C 965	12.4	88.6	4883	6	US-10-128-714-429	Sequence 429, App
C 893	12.4	88.6	2192	8	US-10-425-114-33576	Sequence 33576, App	C 966	12.4	88.6	4884	6	US-10-128-714-5429	Sequence 5429, App

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967 12.4 88.6 5438 9 US-10-357-930-24294 Sequence 24294, A
968 12.4 88.6 5761 10 US-10-486-706-259 Sequence 259, App
969 12.4 88.6 5816 10 US-10-764-420-2097 Sequence 2097, Ap
970 12.4 88.6 5977 9 US-10-331-053-82 Sequence 82, Appl
971 12.4 88.6 6106 7 US-10-062-674-1648 Sequence 1648, Ap
972 12.4 88.6 7129 13 US-11-097-143-12904 Sequence 12904, A
973 12.4 88.6 7327 10 US-10-496-011-17 Sequence 17, Appl
974 12.4 88.6 7358 13 US-11-097-143-24706 Sequence 24706, A
975 12.4 88.6 7642 3 US-09-938-842A-43 Sequence 43, Appl
976 12.4 88.6 7642 3 US-09-938-842A-43 Sequence 43, Appl
977 12.4 88.6 7898 10 US-10-483-467-3 Sequence 3, Appli
978 12.4 88.6 10024 3 US-09-880-107-2430 Sequence 2430, Ap
979 12.4 88.6 11831 2 US-08-961-527-65 Sequence 65, Appl
980 12.4 88.6 11841 8 US-10-158-844-65 Sequence 65, Appl
981 12.4 88.6 17042 10 US-10-965-566-5 Sequence 5, Appli
982 12.4 88.6 21142 10 US-10-995-561-13380 Sequence 13380, A
983 12.4 88.6 21739 8 US-10-741-601-5713 Sequence 5713, Ap
984 12.4 88.6 21739 9 US-10-741-600-17817 Sequence 17817, A
985 12.4 88.6 21791 16 US-11-124-367A-5061 Sequence 5061, Ap
986 12.4 88.6 22477 6 US-10-087-192-1594 Sequence 1594, Ap
987 12.4 88.6 29829 6 US-10-087-192-694 Sequence 694, App
988 12.4 88.6 32070 9 US-10-741-600-17732 Sequence 17732, A
989 12.4 88.6 32070 10 US-10-995-561-13317 Sequence 13317, A
990 12.4 88.6 32134 3 US-09-764-847-1057 Sequence 1057, Ap
991 12.4 88.6 32134 3 US-09-764-877-3535 Sequence 3535, Ap
992 12.4 88.6 32134 3 US-09-764-891-6357 Sequence 6357, Ap
993 12.4 88.6 32134 6 US-10-092-154-1057 Sequence 1057, Ap
994 12.4 88.6 32134 6 US-10-205-428-653 Sequence 653, App
995 12.4 88.6 32134 7 US-10-242-515-3535 Sequence 3535, Ap
996 12.4 88.6 32187 3 US-09-764-847-1550 Sequence 1550, Ap
997 12.4 88.6 32187 6 US-10-092-154-1550 Sequence 1550, Ap
998 12.4 88.6 32193 3 US-09-764-847-1549 Sequence 1549, Ap
999 12.4 88.6 32193 6 US-10-092-154-1549 Sequence 1549, Ap
1000 12.4 88.6 32387 15 US-11-124-368A-2887 Sequence 2887, Ap
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ALIGNMENTS

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RESULT 1
US-09-865-579A-17
; Sequence 17, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiko
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
US-09-865-579A-17
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Query Match 100.0%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GAAGGTGTGCTTAC 14
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Db 1 GAAGGTGTGCTTAC 14

RESULT 2

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US-09-865-579A-19
; Sequence 19, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiko
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-19
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Query Match 100.0%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14

Db 1 GAAGGTGTGCTTAC 14

RESULT 3

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US-10-735-357-44/c
; Sequence 44, Application US/10735357
; Publication No. US20050059030A1
; GENERAL INFORMATION:
; APPLICANT: Bao, Yijia P.
; APPLICANT: Marla, Sudhakar S.
; APPLICANT: Muller, Uwe
; APPLICANT: Storchoff, James J.
; APPLICANT: Hagenow, Susan R.
; TITLE OF INVENTION: Direct SNP Detection with Unamplified DNA
; FILE REFERENCE: 02-1227-A
; CURRENT APPLICATION NUMBER: US/10/735,357
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/432,772
; PRIOR FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: US 60/433,442
; PRIOR FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-357-44
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Query Match 100.0%; Score 14; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

Db 20 GAAGGTGTGCTTAC 7

RESULT 4

US-10-735-357-75

; Sequence 75, Application US/10735357

; Publication No. US20050059030A1

; GENERAL INFORMATION:

; APPLICANT: Bao, Yijia P.

; APPLICANT: Maria, Sudhakar S.

; APPLICANT: Muller, Uwe

; APPLICANT: Storhoff, James J.

; APPLICANT: Hagenow, Susan R.

; TITLE OF INVENTION: Direct SNP Detection with Unamplified DNA

; FILE REFERENCE: 02-1227-A

; CURRENT APPLICATION NUMBER: US/10/735,357

; CURRENT FILING DATE: 2003-12-12

; PRIOR APPLICATION NUMBER: US 60/432,772

; PRIOR FILING DATE: 2002-12-12

; PRIOR APPLICATION NUMBER: US 60/433,442

; PRIOR FILING DATE: 2002-12-12

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 75

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide

US-10-735-357-75

Query Match 100.0%; Score 14; DB 10; Length 22;

Best Local Similarity 100.0%; Pred. No. 8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

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Db 3 GAAGGTGTGCTTAC 16

RESULT 5

US-10-995-051-16/c

; Sequence 16, Application US/10995051

; Publication No. US20050250094A1

; GENERAL INFORMATION:

; APPLICANT: Storhoff, James

; APPLICANT: Lucas, Adam

; APPLICANT: Muller, Uwe

; APPLICANT: Bao, Yijia P

; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination

; FILE REFERENCE: MBHB-03-466-E

; CURRENT APPLICATION NUMBER: US/10/995,051

; CURRENT FILING DATE: 2004-11-22

; PRIOR APPLICATION NUMBER: 10/854,848

; PRIOR FILING DATE: 2004-05-27

; PRIOR APPLICATION NUMBER: 60/474,569

; PRIOR FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 60/499,034

; PRIOR FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 60/517,450

; PRIOR FILING DATE: 2003-11-04

; PRIOR APPLICATION NUMBER: 60/567,874

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 16

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Probe meca 4 for the meca gene.

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(1)

; OTHER INFORMATION: g is linked to SEQ ID NO: 32 by polyethylene glycol

US-10-995-051-16

Query Match

Best Local Similarity 100.0%; Score 14; DB 10; Length 22;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

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Db 20 GAAGGTGTGCTTAC 7

RESULT 6

US-10-995-051-14/c

; Sequence 14, Application US/10995051

; Publication No. US20050250094A1

; GENERAL INFORMATION:

; APPLICANT: Storhoff, James

; APPLICANT: Lucas, Adam

; APPLICANT: Muller, Uwe

; APPLICANT: Bao, Yijia P

; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination

; FILE REFERENCE: MBHB-03-466-E

; CURRENT APPLICATION NUMBER: US/10/995,051

; CURRENT FILING DATE: 2004-11-22

; PRIOR APPLICATION NUMBER: 10/854,848

; PRIOR FILING DATE: 2004-05-27

; PRIOR APPLICATION NUMBER: 60/474,569

; PRIOR FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 60/499,034

; PRIOR FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 60/517,450

; PRIOR FILING DATE: 2003-11-04

; PRIOR APPLICATION NUMBER: 60/567,874

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 14

; LENGTH: 281

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Target Meca 4 is a meca 281 base-pair PCR amplicon.

US-10-995-051-14

Query Match

Best Local Similarity 100.0%; Score 14; DB 10; Length 281;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

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Db 47 GAAGGTGTGCTTAC 34

RESULT 7

US-10-478-633A-151/c

; Sequence 151, Application US/10478633A

; Publication No. US20050059000A1

; GENERAL INFORMATION:

; APPLICANT: TAKARA BIO INC.

; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for

; FILE REFERENCE: 663232

; CURRENT APPLICATION NUMBER: US/10/478,633A

; CURRENT FILING DATE: 2003-11-25

; PRIOR APPLICATION NUMBER: JP 2001-177737

; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: JP 2001-249689

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 173

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; SEQ ID NO 151
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-151

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Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 74 GAAGGTGTGCTTAC 61

RESULT 8
US-10-027-632-152712
; Sequence 152712, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152712
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-152712

Query Match      100.0%; Score 14; DB 6; Length 738;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 699 GAAGGTGTGCTTAC 712

RESULT 9
US-10-027-632-152713
; Sequence 152713, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152713
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-152713

Query Match      100.0%; Score 14; DB 6; Length 738;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 699 GAAGGTGTGCTTAC 712

RESULT 10
US-10-027-632-152712
; Sequence 152712, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152712
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-152712

Query Match      100.0%; Score 14; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 699 GAAGGTGTGCTTAC 712

RESULT 11
US-10-027-632-152713
; Sequence 152713, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152713
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-152713

Query Match 100.0%; Score 14; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 9e+02; 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14
|||||
Db 699 GAAGGTGCTTAC 712

RESULT 12
US-10-425-114-2665/c
; Sequence 2665, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2665
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700220675_FLI
US-10-425-114-2665

Query Match 100.0%; Score 14; DB 8; Length 1502;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14
|||||
Db 618 GAAGGTGCTTAC 605

RESULT 13
US-10-425-115-102549/c

; Sequence 102549, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 102549
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_25033C.1
US-10-425-115-102549

Query Match 100.0%; Score 14; DB 9; Length 1502;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14
|||||
Db 618 GAAGGTGCTTAC 605

RESULT 14
US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match 100.0%; Score 14; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14
|||||
Db 1044 GAAGGTGCTTAC 1031

RESULT 15
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match 100.0%; Score 14; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1 GAAGGTGTGCTTAC 14
|||
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 16
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match 100.0%; Score 14; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1 GAAGGTGTGCTTAC 14
|||
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 17
US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match 100.0%; Score 14; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1 GAAGGTGTGCTTAC 14
|||
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 18
US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match 100.0%; Score 14; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1 GAAGGTGTGCTTAC 14
|||
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 19
US-10-479-674-91/c
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match 100.0%; Score 14; DB 9; Length 2007;

Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 1094 GAAGGTGTGCTTAC 1081

RESULT 20

US-10-121-120-169/c

; Sequence 169, Application US/10121120

; Publication No. US20050042606A9

; GENERAL INFORMATION:

; APPLICANT: Bergeron, Michel G.

; APPLICANT: Ouellette, Marc

; APPLICANT: Roy, Paul H.

; TITLE OF INVENTION: Specific and Universal Probes and Amplification

; TITLE OF INVENTION: Primers

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial

; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical

; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

; FILE REFERENCE: 12287.31

; CURRENT APPLICATION NUMBER: US/10/121,120

; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: 09/452,599

; PRIOR FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: 08/304,732

; PRIOR FILING DATE: 1994-09-12

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 169

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-121-120-169

Query Match

100.0%;

Score 14; DB 9; Length 2007;

Best Local Similarity

100.0%;

Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 1094 GAAGGTGTGCTTAC 1081

RESULT 21

US-10-320-797-1231/c

; Sequence 1231, Application US/10320797

; Publication No. US20040014955A1

; GENERAL INFORMATION:

; APPLICANT: Eroshkin, Alexey M.

; APPLICANT: Zamudio, Carlos

; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND

; TITLE OF INVENTION: METHODS OF USE

; FILE REFERENCE: 10182-021-999

; CURRENT APPLICATION NUMBER: US/10/320,797

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: 60/341,261

; PRIOR FILING DATE: 2001-12-17

; NUMBER OF SEQ ID NOS: 3361

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1231

; LENGTH: 2015

; TYPE: DNA

; ORGANISM: Cryptococcus neoformans

US-10-320-797-1231

Query Match

100.0%;

Score 14; DB 8; Length 2015;

Best Local Similarity

100.0%;

Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 1034 GAAGGTGTGCTTAC 1021

RESULT 22

US-10-724-972A-3141/c

; Sequence 3141, Application US/10724972A

; Publication No. US20040147734A1

; GENERAL INFORMATION:

; APPLICANT: Doucette-Stamm, Lynn

; APPLICANT: Bush, David

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: PATH03-16

; CURRENT APPLICATION NUMBER: US/10/724,972A

; CURRENT FILING DATE: 2003-12-01

; PRIOR APPLICATION NUMBER: 09/450,969

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: 09/134,001

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 7544

; SEQ ID NO 3141

; LENGTH: 2028

; TYPE: DNA

; ORGANISM: S.epidermidis

US-10-724-972A-3141

Query Match

100.0%;

Score 14; DB 8; Length 2028;

Best Local Similarity

100.0%;

Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 1115 GAAGGTGTGCTTAC 1102

RESULT 23

US-10-320-797-231/c

; Sequence 231, Application US/10320797

; Publication No. US20040014955A1

; GENERAL INFORMATION:

; APPLICANT: Eroshkin, Alexey M.

; APPLICANT: Zamudio, Carlos

; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND

; TITLE OF INVENTION: METHODS OF USE

; FILE REFERENCE: 10182-021-999

; CURRENT APPLICATION NUMBER: US/10/320,797

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: 60/341,261

; PRIOR FILING DATE: 2001-12-17

; NUMBER OF SEQ ID NOS: 3361

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 231

; LENGTH: 4015

; TYPE: DNA

; ORGANISM: Cryptococcus neoformans

US-10-320-797-231

Query Match

100.0%;

Score 14; DB 8; Length 4015;

Best Local Similarity

100.0%;

Pred. No. 9.5e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 2034 GAAGGTGTGCTTAC 2021

RESULT 24

US-10-719-900-225680/c

; Sequence 225680, Application US/10719900

```
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 225680
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-225680

Query Match          92.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 14 GAAGGTGTGCTTA 2

RESULT 25
US-11-036-317-858913
; Sequence 858913, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 858913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-858913

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 8 AAGGTGTGCTTAC 20

RESULT 26
US-11-036-317-863503
; Sequence 863503, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 863503
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-863503

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 6 AAGGTGTGCTTAC 18

RESULT 27
US-11-036-317-888398
; Sequence 888398, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 888398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-888398

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 9 AAGGTGTGCTTAC 21

RESULT 28
US-11-036-317-958076
; Sequence 958076, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 958076
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-958076

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 6 AAGGTGTGCTTAC 18

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 6 AAGGTGTGCTTAC 18
```

```
RESULT 29
US-10-741-601-18514
; Sequence 18514, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18514
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-18514

Query Match          92.9%; Score 13; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 38 GAAGGTGTGCTTA 50

RESULT 30
US-10-741-600-50241
; Sequence 50241, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50241
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-50241

Query Match          92.9%; Score 13; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 38 GAAGGTGTGCTTA 50

RESULT 31
US-10-450-763-29551
; Sequence 29551, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
```

```
; SOFTWARE: Custom
; SEQ ID NO 29551
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (78)..(116)
; OTHER INFORMATION: 84% homologous to Escherichia coli rtn, accession number
; OTHER INFORMATION: U83404, Smith-Waterman Score=64.
US-10-450-763-29551

Query Match          92.9%; Score 13; DB 10; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 132 AAGGTGTGCTTAC 144

RESULT 32
US-10-424-599-6873/c
; Sequence 6873, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 6873
; LENGTH: 335
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106214C.1
US-10-424-599-6873

Query Match          92.9%; Score 13; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 21 GAAGGTGTGCTTA 9

RESULT 33
US-09-732-627A-1859
; Sequence 1859, Application US/09732627A
; Publication No. US2004012338A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51770)B
; CURRENT APPLICATION NUMBER: US/09/732,627A
; CURRENT FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 4930
; SEQ ID NO 1859
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(339)
; OTHER INFORMATION: unsure at all n locations
```

```

; OTHER INFORMATION: Clone ID: LIB3493-052-P1-M1-C7
US-09-732-627A-1859

Query Match          92.9%; Score 13; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 13
    |||||
Db 43 GAAGGTGTGCTTAC 55

RESULT 34
US-10-424-599-129096/c
; Sequence 129096, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 129096
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(346)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_87579C.1
US-10-424-599-129096

Query Match          92.9%; Score 13; DB 8; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
    |||||
Db 202 AAGGTGTGCTTAC 190

RESULT 35
US-09-925-065A-201193
; Sequence 201193, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201193
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201193

Query Match          92.9%; Score 13; DB 5; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
    |||||
Db 89 AAGGTGTGCTTAC 101

RESULT 37
US-09-925-065A-201194
; Sequence 201194, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201193
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201193

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201193

Query Match          92.9%; Score 13; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
    |||||
Db 89 AAGGTGTGCTTAC 101

RESULT 36
US-09-925-065A-201193
; Sequence 201193, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201193
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201193

Query Match          92.9%; Score 13; DB 5; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
    |||||
Db 89 AAGGTGTGCTTAC 101

RESULT 37
US-09-925-065A-201194
; Sequence 201194, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201193
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201193

```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201194
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201194

Query Match          92.9%; Score 13; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
      |||||
Db      102 AAGGTGTGCTTAC 114

RESULT 38
US-09-925-065A-201194
; Sequence 201194, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201194
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201194

Query Match          92.9%; Score 13; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
      |||||
Db      102 AAGGTGTGCTTAC 114

RESULT 39
US-10-301-480-289751
; Sequence 289751, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226918
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 289751
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-158432/c
```

```
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-903160

Query Match          92.9%; Score 13; DB 12; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
      |||||
Db      103 AAGGTGTGCTTAC 115

RESULT 40
US-10-301-480-903160
; Sequence 903160, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903160
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-903160

Query Match          92.9%; Score 13; DB 12; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
      |||||
Db      103 AAGGTGTGCTTAC 115

RESULT 41
US-09-925-065A-158432/c
; Sequence 158432, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158432
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-158432
```

Query Match 92.9%; Score 13; DB 4; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
| | | | | | | | | | | | | | |
Db 117 GAAGGTGTGCTTA 105

RESULT 42
US-09-925-065A-158432/c
; Sequence 158432, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158432
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-158432

Query Match 92.9%; Score 13; DB 5; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
| | | | | | | | | | | | | | |
Db 117 GAAGGTGTGCTTA 105

RESULT 43
US-10-437-963-95228
; Sequence 95228, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 95228
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_93443C.1

US-10-437-963-95228

Query Match 92.9%; Score 13; DB 8; Length 459;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
| | | | | | | | | | | | | | |
Db 42 AAGGTGTGCTTAC 54

RESULT 44
US-10-437-963-49273
; Sequence 49273, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49273
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_51871C.1
US-10-437-963-49273

Query Match 92.9%; Score 13; DB 8; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
| | | | | | | | | | | | | | |
Db 119 GAAGGTGTGCTTA 131

RESULT 45
US-09-925-065A-282736
; Sequence 282736, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282736
; LENGTH: 468
; TYPE: DNA

```
; ORGANISM: Homo sapiens
US-09-925-065A-282736

Query Match          92.9%; Score 13; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 128 GAAGGTGTGCTTA 140

RESULT 46
US-09-925-065A-515582/c
; Sequence 515582, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 515582
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-515582

Query Match          92.9%; Score 13; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 431 GAAGGTGTGCTTA 419

RESULT 47
US-09-925-065A-282736
; Sequence 282736, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282736
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-282736
```

```
; SEQ ID NO 282736
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-282736

Query Match          92.9%; Score 13; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 128 GAAGGTGTGCTTA 140

RESULT 48
US-09-925-065A-515582/c
; Sequence 515582, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 515582
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-515582

Query Match          92.9%; Score 13; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 431 GAAGGTGTGCTTA 419

RESULT 49
US-10-301-480-359684
; Sequence 359684, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359684
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; ORGANISM: Homo sapien
US-10-301-480-359684

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; Sequence 973093, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
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; SEQ ID NO 973093
; LENGTH: 474
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; ORGANISM: Homo sapien
US-10-301-480-973093

Query Match          92.9%; Score 13; DB 12; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTA 13
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Search completed: May 31, 2006, 22:06:45
Job time : 1490 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:42:13 ; Search time 57 Seconds
(without alignments)
28.927 Million cell updates/sec

Title: US-09-865-579a-19

Perfect score: 14

Sequence: 1 gaaggtgcttac 14

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA New.*

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- 7: /EMC_Celerra_SIDS3/ptodata/2/pubna/US11_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	12.4	88.6	50	US-10-511-937-2635	Sequence 2635, Ap
C 2	12.4	88.6	765	US-11-217-529-77707	Sequence 77707, A
C 3	12.4	88.6	1019	US-10-953-349-20394	Sequence 20394, A
C 4	12.4	88.6	1161	US-11-217-529-3002	Sequence 3002, Ap
C 5	12.4	88.6	1304	US-10-953-349-8649	Sequence 8649, Ap
C 6	12.4	88.6	1451	US-10-511-937-2804	Sequence 2804, Ap
C 7	12.4	88.6	2079	US-11-217-529-82278	Sequence 82278, A
C 8	12.4	88.6	3435	US-10-953-349-4556	Sequence 4556, Ap
C 9	12.4	88.6	128361	US-10-505-928-151	Sequence 151, App
C 10	12	85.7	650	US-10-953-349-23971	Sequence 23971, A
C 11	12	85.7	651	US-10-953-349-12654	Sequence 12654, A
C 12	12	85.7	951	US-11-217-529-2897	Sequence 2897, Ap
C 13	12	85.7	1212	US-10-953-349-17567	Sequence 17567, A
C 14	12	85.7	1578	US-11-024-544A-17	Sequence 17, Appl
C 15	12	85.7	1578	US-11-190-750-131	Sequence 131, App
C 16	12	85.7	1578	US-11-264-784-83	Sequence 83, Appl
C 17	12	85.7	1578	US-11-264-737-124	Sequence 124, App
C 18	12	85.7	1584	US-11-217-529-84407	Sequence 84407, A
C 19	12	85.7	1667	US-10-953-349-12369	Sequence 12369, A
C 20	12	85.7	1683	US-11-024-544A-156	Sequence 156, App
C 21	12	85.7	1683	US-11-190-750-127	Sequence 127, App
C 22	12	85.7	1749	US-10-953-349-16812	Sequence 16812, A
C 23	12	85.7	1841	US-11-145-207A-163	Sequence 163, App
C 24	12	85.7	3915	US-11-217-529-2644	Sequence 2644, Ap
C 25	12	85.7	8666	US-11-024-544A-165	Sequence 165, App

C 26	12	85.7	8666	7	US-11-264-784-141	Sequence 141, App
C 27	12	85.7	8666	7	US-11-264-737-193	Sequence 193, App
C 28	11.4	81.4	25	7	US-11-217-529-21396	Sequence 21396, A
C 29	11.4	81.4	25	7	US-11-217-529-21401	Sequence 21401, A
C 30	11.4	81.4	25	7	US-11-217-529-68345	Sequence 68345, A
C 31	11.4	81.4	25	7	US-11-217-529-109203	Sequence 109203, A
C 32	11.4	81.4	25	7	US-11-217-529-134611	Sequence 134611, A
C 33	11.4	81.4	357	7	US-11-217-529-1402	Sequence 1402, Ap
C 34	11.4	81.4	393	7	US-11-217-529-5611	Sequence 5611, Ap
C 35	11.4	81.4	429	7	US-11-217-529-79973	Sequence 79973, A
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C 37	11.4	81.4	442	6	US-10-488-619-102	Sequence 102, App
C 38	11.4	81.4	491	6	US-10-488-619-215	Sequence 215, App
C 39	11.4	81.4	513	6	US-10-488-619-637	Sequence 637, App
C 40	11.4	81.4	517	6	US-10-488-619-214	Sequence 214, App
C 41	11.4	81.4	538	6	US-10-953-349-6188	Sequence 6188, Ap
C 42	11.4	81.4	545	6	US-10-488-619-636	Sequence 636, App
C 43	11.4	81.4	547	6	US-10-488-619-202	Sequence 202, App
C 44	11.4	81.4	561	6	US-10-488-619-2061	Sequence 2061, Ap
C 45	11.4	81.4	592	6	US-10-488-619-1924	Sequence 1924, Ap
C 46	11.4	81.4	609	7	US-11-217-529-2	Sequence 2, Appl1
C 47	11.4	81.4	609	7	US-11-217-529-1593	Sequence 1593, Ap
C 48	11.4	81.4	668	6	US-10-488-619-2060	Sequence 2060, Ap
C 49	11.4	81.4	711	6	US-10-488-619-1923	Sequence 1923, Ap
C 50	11.4	81.4	840	7	US-11-249-111-37	Sequence 37, Appl
C 51	11.4	81.4	882	7	US-11-217-529-537	Sequence 537, App
C 52	11.4	81.4	888	7	US-11-217-529-76032	Sequence 76032, A
C 53	11.4	81.4	915	7	US-11-217-529-78711	Sequence 78711, A
C 54	11.4	81.4	978	7	US-11-217-529-75366	Sequence 75366, A
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C 57	11.4	81.4	1107	7	US-11-217-529-76437	Sequence 76437, A
C 58	11.4	81.4	1184	7	US-11-122-986-310	Sequence 310, App
C 59	11.4	81.4	1188	7	US-11-122-986-310	Sequence 310, App
C 60	11.4	81.4	1194	7	US-11-121-154-138	Sequence 138, App
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C 62	11.4	81.4	1359	6	US-10-953-349-21254	Sequence 21254, A
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C 67	11.4	81.4	1545	6	US-10-795-135-4	Sequence 4, Appl1
C 68	11.4	81.4	1549	6	US-10-953-349-28841	Sequence 28841, A
C 69	11.4	81.4	1614	6	US-10-953-349-1483	Sequence 1483, A
C 70	11.4	81.4	1699	6	US-10-953-349-31849	Sequence 31849, A
C 71	11.4	81.4	1729	6	US-10-953-349-33639	Sequence 33639, A
C 72	11.4	81.4	1762	6	US-10-953-349-8359	Sequence 8359, Ap
C 73	11.4	81.4	1798	6	US-10-953-349-5065	Sequence 5065, Ap
C 74	11.4	81.4	1798	6	US-10-953-349-5431	Sequence 5431, Ap
C 75	11.4	81.4	1833	7	US-11-217-529-4925	Sequence 4925, Ap
C 76	11.4	81.4	1841	6	US-10-953-349-16988	Sequence 16988, A
C 77	11.4	81.4	1887	7	US-11-217-529-2426	Sequence 2426, Ap
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C 81	11.4	81.4	2161	7	US-11-075-398-10	Sequence 10, Appl
C 82	11.4	81.4	2243	7	US-11-293-697-405	Sequence 405, App
C 83	11.4	81.4	2326	7	US-11-024-544A-7	Sequence 7, Appl1
C 84	11.4	81.4	2326	7	US-11-190-750-59	Sequence 59, Appl
C 85	11.4	81.4	2326	7	US-11-264-784-76	Sequence 76, Appl
C 86	11.4	81.4	2326	7	US-11-264-737-117	Sequence 117, App
C 87	11.4	81.4	2333	7	US-11-293-697-1519	Sequence 1519, Ap
C 88	11.4	81.4	2400	6	US-10-511-937-2827	Sequence 2827, Ap
C 89	11.4	81.4	2567	7	US-11-293-697-90	Sequence 90, Appl
C 90	11.4	81.4	2588	7	US-11-293-697-614	Sequence 614, App
C 91	11.4	81.4	2663	6	US-10-953-349-4935	Sequence 4935, Ap
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C 93	11.4	81.4	2720	6	US-10-196-749-137	Sequence 137, App
C 94	11.4	81.4	2769	7	US-11-293-697-397	Sequence 397, App
C 95	11.4	81.4	2883	7	US-11-217-529-76512	Sequence 76512, A
C 96	11.4	81.4	2934	7	US-11-217-529-79433	Sequence 79433, A
C 97	11.4	81.4	3129	6	US-10-548-484-52	Sequence 52, Appl
C 98	11.4	81.4	3273	7	US-11-217-529-80828	Sequence 80828, A

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c 101	11.4	81.4	3510	6	US-10-505-928-752	Sequence 752, App	174	10.8	77.1	976	7	US-10-953-349-40094	Sequence 40094, A
c 102	11.4	81.4	3510	6	US-10-511-937-392	Sequence 392, App	175	10.8	77.1	984	7	US-11-217-529-79124	Sequence 79124, A
c 103	11.4	81.4	3937	6	US-10-713-648A-23	Sequence 23, Appl	176	10.8	77.1	990	7	US-11-217-529-171	Sequence 171, App
c 104	11.4	81.4	5262	7	US-11-217-529-786	Sequence 786, App	c 177	10.8	77.1	991	6	US-10-953-349-29815	Sequence 29815, A
c 105	11.4	81.4	5307	6	US-10-505-928-824	Sequence 824, Appl	c 178	10.8	77.1	995	6	US-10-511-937-573	Sequence 573, App
c 106	11.4	81.4	6809	6	US-10-713-648A-24	Sequence 24, Appl	c 179	10.8	77.1	1022	6	US-10-953-349-39353	Sequence 39353, A
c 107	11.4	81.4	6974	6	US-10-505-928-673	Sequence 673, App	c 180	10.8	77.1	1038	7	US-11-217-529-76808	Sequence 76808, A
c 108	11.4	81.4	27419	6	US-10-857-260-34	Sequence 34, Appl	c 181	10.8	77.1	1053	7	US-11-217-529-559	Sequence 559, App
c 109	11	78.6	25	7	US-11-217-529-113164	Sequence 113164, A	c 182	10.8	77.1	1053	7	US-10-953-349-37161	Sequence 37161, A
c 110	11	78.6	597	7	US-11-217-529-78058	Sequence 78058, A	c 183	10.8	77.1	1116	6	US-10-953-349-2827	Sequence 2827, Ap
c 111	11	78.6	1083	7	US-11-217-529-2210	Sequence 2210, Ap	c 184	10.8	77.1	1123	6	US-10-953-349-9985	Sequence 9985, Ap
c 112	11	78.6	1095	7	US-11-217-529-155	Sequence 150, App	c 185	10.8	77.1	1133	6	US-11-217-529-80320	Sequence 80320, A
c 113	11	78.6	1269	7	US-11-217-529-3899	Sequence 3899, Ap	c 186	10.8	77.1	1137	7	US-10-196-749-9	Sequence 9, Appl
c 114	11	78.6	1695	7	US-11-217-529-75761	Sequence 75761, A	c 187	10.8	77.1	1173	6	US-11-101-316-1	Sequence 1, Appl
c 115	11	78.6	1899	6	US-10-953-349-26010	Sequence 26010, A	c 188	10.8	77.1	1174	6	US-10-953-349-20773	Sequence 20773, A
c 116	11	78.6	1974	7	US-11-217-529-1733	Sequence 1733, Ap	c 189	10.8	77.1	1178	6	US-10-953-349-19188	Sequence 19188, A
c 117	11	78.6	2278	7	US-11-293-697-1414	Sequence 1414, Ap	c 190	10.8	77.1	1185	7	US-11-217-529-2974	Sequence 2974, Ap
c 118	11	78.6	2296	6	US-10-953-349-31463	Sequence 31463, A	c 191	10.8	77.1	1203	6	US-11-217-529-4104	Sequence 4104, Ap
c 119	11	78.6	2322	7	US-11-293-697-657	Sequence 657, App	c 192	10.8	77.1	1206	7	US-11-217-529-5992	Sequence 5992, Ap
c 120	11	78.6	2336	7	US-11-293-697-330	Sequence 330, App	c 193	10.8	77.1	1218	7	US-11-217-529-80524	Sequence 80524, A
c 121	11	78.6	2361	7	US-11-317-329-11	Sequence 11, Appl	c 194	10.8	77.1	1221	7	US-11-217-529-2625	Sequence 2625, Ap
c 122	11	78.6	2400	7	US-11-217-529-77227	Sequence 77227, A	c 195	10.8	77.1	1224	6	US-11-217-529-2625	Sequence 2625, Ap
c 123	11	78.6	3466	7	US-11-293-697-718	Sequence 718, App	c 196	10.8	77.1	1236	7	US-11-217-529-3380	Sequence 3380, Ap
c 124	11	78.6	4887	7	US-11-217-529-2955	Sequence 2955, Ap	c 197	10.8	77.1	1236	7	US-11-217-529-3380	Sequence 3380, Ap
c 125	11	78.6	5376	7	US-11-313-450-17	Sequence 17, Appl	c 198	10.8	77.1	1262	6	US-10-473-173-99	Sequence 99, Appl
c 126	10.8	77.1	25	7	US-11-217-529-16559	Sequence 16559, A	c 199	10.8	77.1	1269	6	US-11-217-529-166648	Sequence 166648, A
c 127	10.8	77.1	25	7	US-11-217-529-36857	Sequence 36857, A	c 200	10.8	77.1	1271	6	US-10-953-349-1962	Sequence 1962, Ap
c 128	10.8	77.1	25	7	US-11-217-529-49997	Sequence 49997, A	c 201	10.8	77.1	1271	6	US-10-953-349-1962	Sequence 1962, Ap
c 129	10.8	77.1	25	7	US-11-217-529-51478	Sequence 51478, A	c 202	10.8	77.1	1275	6	US-11-217-529-7815	Sequence 7815, A
c 130	10.8	77.1	25	7	US-11-217-529-110435	Sequence 110435, A	c 203	10.8	77.1	1314	6	US-10-953-349-25175	Sequence 25175, A
c 131	10.8	77.1	25	7	US-11-217-529-135965	Sequence 135965, A	c 204	10.8	77.1	1317	6	US-11-217-529-2100	Sequence 2100, Ap
c 132	10.8	77.1	25	7	US-11-217-529-135974	Sequence 135974, A	c 205	10.8	77.1	1319	6	US-10-953-349-25548	Sequence 25548, A
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c 134	10.8	77.1	25	7	US-11-217-529-180882	Sequence 180882, A	c 207	10.8	77.1	1329	7	US-11-217-529-2370	Sequence 2370, Ap
c 135	10.8	77.1	213	7	US-11-217-529-80096	Sequence 80096, A	c 208	10.8	77.1	1329	7	US-11-217-529-2913	Sequence 2913, Ap
c 136	10.8	77.1	255	7	US-11-217-529-3973	Sequence 3973, Ap	c 209	10.8	77.1	1332	7	US-11-217-529-4198	Sequence 4198, Ap
c 137	10.8	77.1	312	7	US-11-301-554-43	Sequence 43, Appl	c 210	10.8	77.1	1332	7	US-11-217-529-78121	Sequence 78121, A
c 138	10.8	77.1	312	7	US-11-217-529-173699	Sequence 173699, A	c 211	10.8	77.1	1335	6	US-10-953-349-19068	Sequence 19068, A
c 139	10.8	77.1	357	7	US-11-217-529-1403	Sequence 1403, Ap	c 212	10.8	77.1	1350	7	US-11-217-529-3041	Sequence 3041, Ap
c 140	10.8	77.1	452	6	US-10-488-619-954	Sequence 954, App	c 213	10.8	77.1	1350	6	US-10-953-349-35101	Sequence 35101, A
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c 143	10.8	77.1	543	7	US-11-217-529-5827	Sequence 5827, Ap	c 216	10.8	77.1	1392	7	US-11-217-529-80238	Sequence 80238, A
c 144	10.8	77.1	560	6	US-10-488-619-1952	Sequence 1952, Ap	c 217	10.8	77.1	1392	7	US-11-122-986-240	Sequence 240, App
c 145	10.8	77.1	573	6	US-10-953-349-30400	Sequence 30400, A	c 218	10.8	77.1	1395	7	US-11-122-986-238	Sequence 238, App
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c 147	10.8	77.1	653	6	US-10-953-349-12260	Sequence 12260, A	c 220	10.8	77.1	1443	7	US-11-217-529-2268	Sequence 2268, Ap
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c 150	10.8	77.1	669	6	US-10-953-349-26927	Sequence 26927, A	c 223	10.8	77.1	1471	6	US-10-953-349-18869	Sequence 18869, A
c 151	10.8	77.1	678	6	US-10-488-619-2734	Sequence 2734, Ap	c 224	10.8	77.1	1471	6	US-11-217-529-77111	Sequence 77111, A
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c 155	10.8	77.1	777	7	US-11-217-529-80790	Sequence 80790, A	c 228	10.8	77.1	1530	7	US-11-217-529-2013	Sequence 2013, Ap
c 156	10.8	77.1	783	7	US-11-217-529-800	Sequence 800, App	c 229	10.8	77.1	1535	6	US-10-953-349-15855	Sequence 15855, A
c 157	10.8	77.1	783	7	US-11-217-529-1054	Sequence 1054, Ap	c 230	10.8	77.1	1540	6	US-10-953-349-26656	Sequence 26656, A
c 158	10.8	77.1	787	7	US-11-217-529-75859	Sequence 75859, A	c 231	10.8	77.1	1542	7	US-11-181-115-21	Sequence 21, Appl
c 159	10.8	77.1	807	6	US-10-488-619-2354	Sequence 2354, Ap	c 232	10.8	77.1	1544	6	US-10-953-349-4088	Sequence 4088, Ap
c 160	10.8	77.1	810	7	US-11-217-529-965	Sequence 965, App	c 233	10.8	77.1	1564	7	US-10-953-349-29884	Sequence 29884, A
c 161	10.8	77.1	816	6	US-10-953-349-35070	Sequence 35070, A	c 234	10.8	77.1	1567	7	US-11-293-697-1059	Sequence 1059, Ap
c 162	10.8	77.1	828	6	US-10-953-349-16551	Sequence 16551, A	c 235	10.8	77.1	1619	6	US-10-953-349-3744	Sequence 3744, A
c 163	10.8	77.1	836	6	US-10-953-349-14414	Sequence 14414, A	c 236	10.8	77.1	1641	6	US-10-953-349-40249	Sequence 40249, A
c 164	10.8	77.1	850	6	US-10-953-349-15270	Sequence 15270, A	c 237	10.8	77.1	1650	7	US-11-217-529-81956	Sequence 81956, A
c 165	10.8	77.1	855	6	US-10-514-535-1	Sequence 1, Appl	c 238	10.8	77.1	1684	7	US-11-293-697-63	Sequence 63, Appl
c 166	10.8	77.1	861	7	US-11-217-529-78673	Sequence 78673, A	c 239	10.8	77.1	1695	6	US-10-953-349-32444	Sequence 32444, A
c 167	10.8	77.1	865	6	US-10-953-349-8546	Sequence 8546, Ap	c 240	10.8	77.1	1706	6	US-10-953-349-36924	Sequence 36924, A
c 168	10.8	77.1	870	6	US-10-953-349-139	Sequence 139, App	c 241	10.8	77.1	1707	7	US-11-217-529-76843	Sequence 76843, A
c 169	10.8	77.1	870	7	US-11-101-316-25	Sequence 25, Appl	c 242	10.8	77.1	1719	7	US-11-217-529-80736	Sequence 80736, A
c 170	10.8	77.1	875	6	US-10-514-535-2	Sequence 2, Appl	c 243	10.8	77.1	1720	6	US-10-953-349-32176	Sequence 32176, A
c 171	10.8	77.1	897	7	US-11-217-529-2796	Sequence 2796, Ap	c 244	10.8	77.1	1722	7	US-11-217-529-3909	Sequence 3909, Ap

c 245	77.1	1725	7	US-11-121-154-50	Sequence 50, Appl	318	10.8	77.1	5920	7	US-11-145-307A-185	Sequence 185, App
c 246	77.1	1750	6	US-10-953-349-34792	Sequence 34792, A	c 319	10.8	77.1	6631	6	US-10-713-648A-22	Sequence 22, Appl
c 247	77.1	1767	6	US-10-953-349-8450	Sequence 8450, App	c 320	10.8	77.1	6721	6	US-10-713-648A-5	Sequence 5, Appl1
c 248	77.1	1785	7	US-11-217-529-77319	Sequence 77319, A	c 321	10.8	77.1	10574	7	US-11-267-871-719	Sequence 719, App
c 249	77.1	1797	7	US-11-217-529-80787	Sequence 80787, A	c 322	10.8	77.1	135090	6	US-10-505-928-607	Sequence 607, App
c 250	77.1	1803	7	US-11-217-529-2767	Sequence 2767, Ap	c 323	10.8	77.1	394191	6	US-10-506-549-3	Sequence 3, Appl1
c 251	77.1	1810	6	US-10-953-349-10986	Sequence 10986, A	c 324	10.4	74.3	22	7	US-11-248-986-23	Sequence 23, Appl
c 252	77.1	1866	7	US-11-121-154-10	Sequence 10, Appl	c 325	10.4	74.3	25	7	US-11-217-529-16665	Sequence 16665, A
c 253	77.1	1872	7	US-11-217-529-1367	Sequence 1367, Ap	c 326	10.4	74.3	25	7	US-11-217-529-19558	Sequence 19558, A
c 254	77.1	1878	7	US-11-217-529-2508	Sequence 2508, Ap	c 327	10.4	74.3	25	7	US-11-217-529-20016	Sequence 20016, A
c 255	77.1	1880	6	US-10-953-349-29344	Sequence 29344, A	c 328	10.4	74.3	25	7	US-11-217-529-20081	Sequence 20081, A
c 256	77.1	1896	6	US-10-953-349-26191	Sequence 26191, A	c 329	10.4	74.3	25	7	US-11-217-529-21404	Sequence 21404, A
c 257	77.1	1950	7	US-11-217-529-3485	Sequence 3485, Ap	c 330	10.4	74.3	25	7	US-11-217-529-106469	Sequence 106469, A
c 258	77.1	1968	7	US-11-293-697-2283	Sequence 2283, Ap	c 331	10.4	74.3	25	7	US-11-217-529-107771	Sequence 107771, A
c 259	77.1	2070	6	US-10-509-131-37	Sequence 37, Appl	c 332	10.4	74.3	25	7	US-11-217-529-110946	Sequence 110946, A
c 260	77.1	2117	7	US-11-293-697-573	Sequence 573, Appl	c 333	10.4	74.3	25	7	US-11-217-529-121489	Sequence 121489, A
c 261	77.1	2142	7	US-11-217-529-36	Sequence 36, Appl	c 334	10.4	74.3	25	7	US-11-217-529-149644	Sequence 149644, A
c 262	77.1	2178	7	US-11-217-529-191034	Sequence 191034, A	c 335	10.4	74.3	25	7	US-11-217-529-153219	Sequence 153219, A
c 263	77.1	2181	7	US-11-293-697-1647	Sequence 1647, Ap	c 336	10.4	74.3	25	7	US-11-217-529-176667	Sequence 176667, A
c 264	77.1	2184	7	US-11-217-529-166643	Sequence 166643, A	c 337	10.4	74.3	25	7	US-11-217-529-176669	Sequence 176669, A
c 265	77.1	2267	7	US-11-266-446-40	Sequence 446, Ap	c 338	10.4	74.3	25	7	US-11-217-529-176672	Sequence 176672, A
c 266	77.1	2267	7	US-11-217-529-77716	Sequence 77716, A	c 339	10.4	74.3	25	7	US-11-217-529-176674	Sequence 176674, A
c 267	77.1	2287	7	US-11-293-697-1973	Sequence 1973, Ap	c 340	10.4	74.3	51	7	US-11-245-248-272	Sequence 272, App
c 268	77.1	2356	7	US-11-293-697-1705	Sequence 1705, Ap	c 341	10.4	74.3	93	7	US-11-217-529-173314	Sequence 173314, A
c 269	77.1	2363	7	US-11-293-697-1688	Sequence 1688, Ap	c 342	10.4	74.3	144	7	US-11-217-529-3905	Sequence 3905, Ap
c 270	77.1	2366	6	US-10-196-749-309	Sequence 309, App	c 343	10.4	74.3	151	7	US-11-320-481-16	Sequence 476, Appl
c 271	77.1	2436	7	US-11-101-316-99	Sequence 99, Appl	c 344	10.4	74.3	197	6	US-10-473-173-476	Sequence 173, App
c 272	77.1	2460	7	US-11-217-529-174454	Sequence 174454, A	c 345	10.4	74.3	288	7	US-11-217-529-263	Sequence 263, App
c 273	77.1	2463	7	US-11-293-697-5	Sequence 5, Appl1	c 346	10.4	74.3	317	6	US-10-488-619-1102	Sequence 1102, Ap
c 274	77.1	2492	7	US-11-293-697-1721	Sequence 1721, Ap	c 347	10.4	74.3	318	7	US-11-321-475-7	Sequence 7, Appl1
c 275	77.1	2529	7	US-11-217-529-4657	Sequence 4657, Ap	c 348	10.4	74.3	354	7	US-11-217-529-77859	Sequence 77859, A
c 276	77.1	2536	7	US-11-293-697-1295	Sequence 1295, Ap	c 349	10.4	74.3	354	7	US-11-217-529-78681	Sequence 78681, A
c 277	77.1	2540	7	US-11-121-154-36	Sequence 36, Appl	c 350	10.4	74.3	363	7	US-11-217-529-81538	Sequence 81538, A
c 278	77.1	2547	6	US-10-953-349-9185	Sequence 9185, Ap	c 351	10.4	74.3	374	6	US-10-488-619-1951	Sequence 1951, Ap
c 279	77.1	2589	7	US-11-121-154-38	Sequence 38, Appl	c 352	10.4	74.3	399	7	US-11-217-529-81634	Sequence 81634, A
c 280	77.1	2589	7	US-11-293-697-616	Sequence 616, App	c 353	10.4	74.3	402	6	US-10-488-619-742	Sequence 742, App
c 281	77.1	2659	7	US-11-293-697-1193	Sequence 1193, Ap	c 354	10.4	74.3	405	7	US-11-301-554-180	Sequence 180, A
c 282	77.1	2751	7	US-11-293-697-815	Sequence 815, App	c 355	10.4	74.3	434	7	US-11-217-529-81704	Sequence 81704, A
c 283	77.1	2822	6	US-10-953-349-9753	Sequence 9753, Ap	c 356	10.4	74.3	486	7	US-11-217-529-166749	Sequence 166749, A
c 284	77.1	2823	7	US-11-217-529-4032	Sequence 4032, Ap	c 357	10.4	74.3	488	6	US-10-953-349-36206	Sequence 36206, A
c 285	77.1	2826	7	US-11-293-697-2347	Sequence 2347, Ap	c 358	10.4	74.3	491	6	US-10-488-619-624	Sequence 624, App
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c 288	77.1	2985	6	US-10-953-349-32829	Sequence 32829, A	c 361	10.4	74.3	549	7	US-11-217-529-1910	Sequence 1910, Ap
c 289	77.1	2988	7	US-11-217-529-2172	Sequence 2172, Ap	c 362	10.4	74.3	585	6	US-10-488-619-1220	Sequence 1220, Ap
c 290	77.1	3032	6	US-10-514-535-7	Sequence 7, Appl1	c 363	10.4	74.3	605	6	US-10-473-173-313	Sequence 313, App
c 291	77.1	3161	7	US-11-293-697-1992	Sequence 1992, Ap	c 364	10.4	74.3	609	7	US-11-217-529-82003	Sequence 82003, A
c 292	77.1	3190	7	US-11-293-697-323	Sequence 323, App	c 365	10.4	74.3	630	6	US-10-953-349-26350	Sequence 26350, A
c 293	77.1	3219	7	US-11-217-529-82170	Sequence 82170, A	c 366	10.4	74.3	642	7	US-11-217-529-78763	Sequence 78763, A
c 294	77.1	3225	7	US-11-217-529-77049	Sequence 77049, A	c 367	10.4	74.3	648	7	US-11-217-529-1283	Sequence 1283, Ap
c 295	77.1	3239	6	US-10-505-928-294	Sequence 294, App	c 368	10.4	74.3	660	7	US-11-217-529-570	Sequence 570, App
c 296	77.1	3243	7	US-11-217-529-80372	Sequence 80372, A	c 369	10.4	74.3	663	7	US-11-226-605-47	Sequence 47, Appl
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c 298	77.1	3357	7	US-11-217-529-80104	Sequence 80104, A	c 371	10.4	74.3	666	6	US-10-953-349-8273	Sequence 8273, Ap
c 299	77.1	3364	7	US-11-293-697-1320	Sequence 1320, Ap	c 372	10.4	74.3	667	6	US-10-488-619-2859	Sequence 2859, Ap
c 300	77.1	3374	6	US-10-514-535-5	Sequence 5, Appl1	c 373	10.4	74.3	669	6	US-10-473-173-31	Sequence 31, Appl
c 301	77.1	3485	7	US-11-145-307A-192	Sequence 192, App	c 374	10.4	74.3	678	7	US-11-217-529-75902	Sequence 75902, A
c 302	77.1	3578	6	US-10-509-131-49	Sequence 49, Appl	c 375	10.4	74.3	701	6	US-10-488-619-2098	Sequence 2098, Ap
c 303	77.1	3585	7	US-11-217-529-1567	Sequence 1567, Ap	c 376	10.4	74.3	702	7	US-11-217-529-4708	Sequence 4708, Ap
c 304	77.1	3733	6	US-10-514-535-3	Sequence 3, Appl1	c 377	10.4	74.3	704	7	US-11-301-554-206	Sequence 206, App
c 305	77.1	3743	6	US-10-502-993-1	Sequence 1, Appl1	c 378	10.4	74.3	708	6	US-10-953-349-14041	Sequence 14041, A
c 306	77.1	3780	6	US-10-509-131-24	Sequence 24, Appl	c 379	10.4	74.3	716	6	US-10-953-349-30224	Sequence 30224, A
c 307	77.1	3786	7	US-11-293-697-436	Sequence 436, App	c 380	10.4	74.3	724	6	US-10-953-349-15117	Sequence 15117, A
c 308	77.1	3787	6	US-10-514-535-4	Sequence 4, Appl1	c 381	10.4	74.3	732	7	US-11-217-529-81607	Sequence 81607, A
c 309	77.1	3801	7	US-11-217-529-4511	Sequence 4511, Ap	c 382	10.4	74.3	748	6	US-10-488-619-2227	Sequence 2227, Ap
c 310	77.1	4008	6	US-10-509-131-39	Sequence 39, Appl	c 383	10.4	74.3	781	6	US-10-953-349-24773	Sequence 24773, A
c 311	77.1	4074	7	US-11-217-529-4467	Sequence 4467, Ap	c 384	10.4	74.3	783	6	US-10-488-619-2102	Sequence 2102, Ap
c 312	77.1	4194	7	US-11-217-529-77339	Sequence 77339, A	c 385	10.4	74.3	817	6	US-10-953-349-18372	Sequence 18372, A
c 313	77.1	4337	7	US-11-293-697-1232	Sequence 1232, Ap	c 386	10.4	74.3	828	7	US-11-217-529-77579	Sequence 77579, A
c 314	77.1	4413	7	US-11-217-529-3933	Sequence 3933, Ap	c 387	10.4	74.3	830	6	US-10-953-349-39705	Sequence 39705, A
c 315	77.1	4894	6	US-10-511-937-566	Sequence 566, App	c 388	10.4	74.3	833	6	US-10-953-349-36674	Sequence 36674, A
c 316	77.1	5217	7	US-11-217-529-5142	Sequence 5142, Ap	c 389	10.4	74.3	876	6	US-10-953-349-21	Sequence 21, Appl
c 317	77.1	5223	7	US-11-217-529-5246	Sequence 5246, Ap	c 390	10.4	74.3	928	6	US-10-953-349-25780	Sequence 25780, A

c 391	10.4	74.3	951	7	US-11-217-529-975	Sequence 975, App	464	10.4	74.3	1629	7	US-11-217-529-77846	Sequence 77846, A
c 392	10.4	74.3	951	7	US-11-217-529-2964	Sequence 2964, App	c 465	10.4	74.3	1641	7	US-11-217-529-78808	Sequence 78808, A
c 393	10.4	74.3	955	6	US-10-488-619-3026	Sequence 3026, App	c 466	10.4	74.3	1717	6	US-10-953-349-32286	Sequence 32286, A
c 394	10.4	74.3	960	7	US-11-217-529-1277	Sequence 1277, App	c 467	10.4	74.3	1727	6	US-10-511-937-457	Sequence 457, App
c 395	10.4	74.3	977	6	US-10-953-349-29094	Sequence 29094, A	c 468	10.4	74.3	1737	7	US-11-217-529-4822	Sequence 4822, App
c 396	10.4	74.3	1003	7	US-11-226-605-12	Sequence 12, Appl	c 469	10.4	74.3	1763	7	US-11-293-697-2150	Sequence 2150, App
c 397	10.4	74.3	1003	7	US-11-226-605-58	Sequence 58, Appl	c 470	10.4	74.3	1811	6	US-11-217-529-76317	Sequence 76317, A
c 398	10.4	74.3	1013	6	US-10-953-349-34990	Sequence 34990, A	c 471	10.4	74.3	1864	6	US-10-953-349-10646	Sequence 10646, A
c 399	10.4	74.3	1014	6	US-10-953-349-19434	Sequence 19434, A	c 472	10.4	74.3	1874	6	US-10-953-349-7064	Sequence 7064, App
c 400	10.4	74.3	1022	6	US-10-953-349-36950	Sequence 36950, A	c 473	10.4	74.3	1829	7	US-11-293-697-1863	Sequence 1863, App
c 401	10.4	74.3	1032	7	US-11-217-529-3044	Sequence 3044, App	c 474	10.4	74.3	1838	7	US-11-293-697-2144	Sequence 2144, App
c 402	10.4	74.3	1039	6	US-10-953-349-27919	Sequence 27919, A	c 475	10.4	74.3	1846	7	US-11-293-697-2144	Sequence 2144, App
c 403	10.4	74.3	1059	7	US-11-217-529-72620	Sequence 72620, A	c 476	10.4	74.3	1848	6	US-10-519-335-5	Sequence 5, Appl
c 404	10.4	74.3	1074	6	US-10-953-349-12809	Sequence 12809, A	c 477	10.4	74.3	1872	7	US-11-217-529-3010	Sequence 3010, App
c 405	10.4	74.3	1078	6	US-10-953-349-14448	Sequence 14448, A	c 478	10.4	74.3	1872	7	US-11-293-697-176	Sequence 176, App
c 406	10.4	74.3	1087	6	US-10-525-647-22	Sequence 22, Appl	c 479	10.4	74.3	1878	6	US-10-519-335-3	Sequence 3, Appl
c 407	10.4	74.3	1101	6	US-10-953-349-36175	Sequence 36175, A	c 480	10.4	74.3	1878	6	US-11-293-697-2381	Sequence 2381, App
c 408	10.4	74.3	1105	6	US-10-953-349-16597	Sequence 16597, A	c 481	10.4	74.3	1881	7	US-11-217-529-5310	Sequence 5310, App
c 409	10.4	74.3	1106	6	US-10-953-349-21891	Sequence 21891, A	c 482	10.4	74.3	1881	7	US-11-217-529-613	Sequence 613, App
c 410	10.4	74.3	1129	6	US-10-953-349-37014	Sequence 37014, A	c 483	10.4	74.3	1899	7	US-11-217-529-613	Sequence 613, App
c 411	10.4	74.3	1141	7	US-11-217-529-131	Sequence 131, App	c 484	10.4	74.3	1902	7	US-11-293-697-2269	Sequence 2269, App
c 412	10.4	74.3	1152	6	US-10-953-349-20671	Sequence 20671, A	c 485	10.4	74.3	1932	6	US-10-519-335-1	Sequence 1, Appl
c 413	10.4	74.3	1160	6	US-10-953-349-18848	Sequence 18848, A	c 486	10.4	74.3	1932	6	US-11-217-529-554	Sequence 554, App
c 414	10.4	74.3	1169	6	US-10-953-349-3649	Sequence 3649, App	c 487	10.4	74.3	1935	7	US-11-217-529-1137	Sequence 1137, App
c 415	10.4	74.3	1184	6	US-10-953-349-21891	Sequence 21891, A	c 488	10.4	74.3	1950	7	US-11-217-529-1907	Sequence 1907, App
c 416	10.4	74.3	1185	6	US-10-953-349-29401	Sequence 29401, A	c 489	10.4	74.3	1956	7	US-11-217-529-4011	Sequence 4011, App
c 417	10.4	74.3	1209	7	US-11-217-529-77464	Sequence 77464, A	c 490	10.4	74.3	1959	6	US-10-953-349-35401	Sequence 35401, A
c 418	10.4	74.3	1212	7	US-11-217-529-370	Sequence 370, App	c 491	10.4	74.3	1992	7	US-11-217-529-5642	Sequence 5642, App
c 419	10.4	74.3	1218	7	US-11-217-529-79983	Sequence 79983, A	c 492	10.4	74.3	1995	6	US-10-953-349-12090	Sequence 12090, A
c 420	10.4	74.3	1220	6	US-10-953-349-18920	Sequence 18920, A	c 493	10.4	74.3	2001	7	US-11-217-529-79229	Sequence 79229, A
c 421	10.4	74.3	1242	6	US-10-953-349-6692	Sequence 6692, App	c 494	10.4	74.3	2008	7	US-11-293-697-75	Sequence 75, Appl
c 422	10.4	74.3	1244	6	US-10-953-349-4128	Sequence 4128, App	c 495	10.4	74.3	2010	7	US-11-217-529-77566	Sequence 77566, A
c 423	10.4	74.3	1254	6	US-10-953-349-3580	Sequence 3580, App	c 496	10.4	74.3	2013	7	US-11-217-529-1571	Sequence 1571, App
c 424	10.4	74.3	1254	6	US-11-217-529-81134	Sequence 81134, A	c 497	10.4	74.3	2016	7	US-11-217-529-82328	Sequence 82328, A
c 425	10.4	74.3	1259	6	US-10-953-349-18783	Sequence 18783, A	c 498	10.4	74.3	2019	7	US-11-293-697-1629	Sequence 1629, App
c 426	10.4	74.3	1275	6	US-11-421-154-102	Sequence 102, App	c 499	10.4	74.3	2024	7	US-11-145-307A-55	Sequence 55, Appl
c 427	10.4	74.3	1278	6	US-10-953-349-24527	Sequence 24527, A	c 500	10.4	74.3	2026	7	US-11-293-697-2111	Sequence 2111, App
c 428	10.4	74.3	1281	7	US-11-217-529-879	Sequence 879, App	c 501	10.4	74.3	2030	7	US-11-322-999-5	Sequence 5, Appl
c 429	10.4	74.3	1282	6	US-10-953-349-29323	Sequence 29323, A	c 502	10.4	74.3	2051	6	US-11-217-529-5680	Sequence 5680, App
c 430	10.4	74.3	1323	6	US-10-505-928-380	Sequence 380, App	c 503	10.4	74.3	2051	6	US-10-953-349-7080	Sequence 7080, App
c 431	10.4	74.3	1332	7	US-11-217-529-77527	Sequence 77527, A	c 504	10.4	74.3	2063	7	US-11-293-697-2390	Sequence 2390, App
c 432	10.4	74.3	1346	6	US-10-953-349-34301	Sequence 34301, A	c 505	10.4	74.3	2077	7	US-11-293-697-1908	Sequence 1908, App
c 433	10.4	74.3	1352	6	US-10-953-349-19492	Sequence 19492, A	c 506	10.4	74.3	2097	7	US-11-301-554-826	Sequence 826, App
c 434	10.4	74.3	1364	6	US-10-953-349-27423	Sequence 27423, A	c 507	10.4	74.3	2109	7	US-11-217-529-3350	Sequence 3350, App
c 435	10.4	74.3	1369	6	US-10-953-349-13239	Sequence 13239, A	c 508	10.4	74.3	2115	7	US-11-293-697-2250	Sequence 2250, App
c 436	10.4	74.3	1369	6	US-10-953-349-22871	Sequence 22871, A	c 509	10.4	74.3	2117	7	US-11-293-697-2421	Sequence 2421, App
c 437	10.4	74.3	1380	6	US-10-953-349-6755	Sequence 6755, App	c 510	10.4	74.3	2131	7	US-11-293-697-1951	Sequence 1951, App
c 438	10.4	74.3	1389	6	US-10-953-349-35006	Sequence 35006, A	c 511	10.4	74.3	2136	7	US-11-318-813-37	Sequence 37, Appl
c 439	10.4	74.3	1401	6	US-10-953-349-21919	Sequence 21919, A	c 512	10.4	74.3	2145	7	US-11-227-644-3	Sequence 3, Appl
c 440	10.4	74.3	1404	7	US-11-217-529-76780	Sequence 76780, A	c 513	10.4	74.3	2146	6	US-10-953-349-5657	Sequence 5657, App
c 441	10.4	74.3	1410	7	US-11-217-529-4030	Sequence 4030, App	c 514	10.4	74.3	2166	7	US-11-217-529-1236	Sequence 1236, App
c 442	10.4	74.3	1417	6	US-10-953-349-26201	Sequence 26201, A	c 515	10.4	74.3	2167	6	US-10-953-349-17117	Sequence 17117, A
c 443	10.4	74.3	1431	7	US-11-217-529-76683	Sequence 76683, A	c 516	10.4	74.3	2184	7	US-11-217-529-5288	Sequence 5288, App
c 444	10.4	74.3	1451	6	US-10-953-349-29115	Sequence 29115, A	c 517	10.4	74.3	2192	7	US-11-293-697-1340	Sequence 1340, App
c 445	10.4	74.3	1480	6	US-10-953-349-31871	Sequence 31871, A	c 518	10.4	74.3	2194	7	US-11-293-697-1951	Sequence 1951, App
c 446	10.4	74.3	1485	7	US-11-217-529-5036	Sequence 5036, App	c 519	10.4	74.3	2214	7	US-11-318-813-1	Sequence 1, Appl
c 447	10.4	74.3	1486	6	US-10-973-274-30	Sequence 30, Appl	c 520	10.4	74.3	2215	7	US-11-293-697-1751	Sequence 1751, App
c 448	10.4	74.3	1500	7	US-11-293-697-1988	Sequence 1988, App	c 521	10.4	74.3	2235	6	US-11-293-697-935	Sequence 935, App
c 449	10.4	74.3	1542	7	US-11-217-529-77984	Sequence 77984, A	c 522	10.4	74.3	2250	6	US-10-953-349-7298	Sequence 7298, App
c 450	10.4	74.3	1553	7	US-11-248-986-25	Sequence 25, Appl	c 523	10.4	74.3	2265	7	US-11-217-529-76346	Sequence 76346, A
c 451	10.4	74.3	1567	7	US-11-293-697-1059	Sequence 1059, App	c 524	10.4	74.3	2349	7	US-11-217-529-3488	Sequence 3488, App
c 452	10.4	74.3	1572	7	US-11-217-529-2215	Sequence 2215, App	c 525	10.4	74.3	2364	6	US-10-953-349-1490	Sequence 1490, App
c 453	10.4	74.3	1582	6	US-10-953-349-32115	Sequence 32115, A	c 526	10.4	74.3	2376	7	US-11-217-529-78788	Sequence 78788, A
c 454	10.4	74.3	1602	7	US-11-217-529-1809	Sequence 1809, App	c 527	10.4	74.3	2391	6	US-11-293-697-1862	Sequence 1862, App
c 455	10.4	74.3	1605	7	US-11-217-529-3550	Sequence 3550, App	c 528	10.4	74.3	2394	6	US-10-953-349-6275	Sequence 6275, App
c 456	10.4	74.3	1607	6	US-10-953-349-11722	Sequence 11722, A	c 529	10.4	74.3	2394	6	US-11-293-697-2296	Sequence 2296, App
c 457	10.4	74.3	1614	6	US-10-953-349-24024	Sequence 24024, A	c 530	10.4	74.3	2403	6	US-10-196-749-45	Sequence 45, Appl
c 458	10.4	74.3	1617	7	US-11-217-529-4915	Sequence 4915, App	c 531	10.4	74.3	2404	7	US-11-293-697-2335	Sequence 2335, App
c 459	10.4	74.3	1618	6	US-10-953-349-13785	Sequence 13785, A	c 532	10.4	74.3	2408	7	US-11-293-697-225	Sequence 225, App
c 460	10.4	74.3	1618	6	US-10-953-349-29520	Sequence 29520, A	c 533	10.4	74.3	2421	7	US-11-217-529-4463	Sequence 4463, App
c 461	10.4	74.3	1619	7	US-11-301-554-801	Sequence 801, App	c 534	10.4	74.3	2455	7	US-11-293-697-411	Sequence 411, App
c 462	10.4	74.3	1625	6	US-10-953-349-17058	Sequence 17058, A	c 535	10.4	74.3	2502	7	US-11-217-529-76658	Sequence 76658, A
c 463	10.4	74.3	1629	7	US-11-227-614-1	Sequence 1, Appl	c 536	10.4	74.3	2507	6	US-10-953-349-9838	Sequence 9838, App
										2534	7	US-11-145-307A-58	Sequence 58, Appl

537	10.4	74.3	2554	7	US-11-193-697-133	Sequence 133, App	c 610	10.4	74.3	12342	7	US-11-217-529-4644	Sequence 4644, App
538	10.4	74.3	2571	6	US-10-196-749-165	Sequence 165, App	611	10.4	74.3	14299	7	US-11-248-986-19	Sequence 19, Appl
539	10.4	74.3	2571	7	US-11-101-316-39	Sequence 39, Appl	612	10.4	74.3	50000	6	US-10-528-659-2	Sequence 2, Appl
540	10.4	74.3	2607	7	US-11-217-529-82366	Sequence 82366, A	613	10.4	74.3	54550	7	US-11-318-813-42	Sequence 42, Appl
541	10.4	74.3	2619	7	US-11-302-678-18	Sequence 18, Appl	614	10.4	74.3	54550	7	US-11-318-813-42	Sequence 42, Appl
542	10.4	74.3	2625	7	US-11-217-529-3881	Sequence 3881, App	615	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
543	10.4	74.3	2634	7	US-11-217-529-80314	Sequence 80314, A	616	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
544	10.4	74.3	2644	7	US-11-266-446-66	Sequence 66, Appl	617	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
545	10.4	74.3	2671	7	US-11-266-446-66	Sequence 66, Appl	618	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
546	10.4	74.3	2676	7	US-11-217-529-5102	Sequence 5102, App	619	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
547	10.4	74.3	2688	7	US-11-293-697-2253	Sequence 2253, App	620	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
548	10.4	74.3	2688	6	US-10-953-349-3061	Sequence 3061, App	621	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
549	10.4	74.3	2690	7	US-11-293-697-1093	Sequence 1093, App	622	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
550	10.4	74.3	2703	7	US-11-217-529-228	Sequence 228, App	623	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
551	10.4	74.3	2760	7	US-11-302-678-63	Sequence 63, Appl	624	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
552	10.4	74.3	2804	7	US-11-293-697-41	Sequence 41, Appl	625	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
553	10.4	74.3	2816	7	US-11-293-697-206	Sequence 206, App	626	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
554	10.4	74.3	2887	7	US-11-293-697-859	Sequence 859, App	627	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
555	10.4	74.3	2907	7	US-11-293-697-282	Sequence 282, App	628	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
556	10.4	74.3	2931	7	US-11-217-529-3493	Sequence 3493, App	629	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
557	10.4	74.3	2995	7	US-11-293-697-600	Sequence 600, App	630	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
558	10.4	74.3	3023	7	US-11-293-697-665	Sequence 665, App	631	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
559	10.4	74.3	3033	6	US-10-196-749-1	Sequence 1, Appl	632	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
560	10.4	74.3	3081	7	US-11-293-697-872	Sequence 872, App	633	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
561	10.4	74.3	3083	7	US-11-242-111-14	Sequence 14, Appl	634	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
562	10.4	74.3	3097	7	US-11-293-697-806	Sequence 806, App	635	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
563	10.4	74.3	3142	7	US-11-254-185-1	Sequence 1, Appl	636	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
564	10.4	74.3	3142	7	US-11-253-869-1	Sequence 1, Appl	637	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
565	10.4	74.3	3174	7	US-11-217-529-427	Sequence 427, App	638	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
566	10.4	74.3	3193	7	US-11-293-697-655	Sequence 655, App	639	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
567	10.4	74.3	3210	7	US-11-217-529-1385	Sequence 1385, App	640	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
568	10.4	74.3	3228	7	US-11-217-529-190982	Sequence 190982, App	641	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
569	10.4	74.3	3232	7	US-11-302-678-16	Sequence 16, Appl	642	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
570	10.4	74.3	3236	7	US-11-293-697-1309	Sequence 1309, App	643	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
571	10.4	74.3	3243	7	US-11-293-697-1332	Sequence 1332, App	644	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
572	10.4	74.3	3246	7	US-11-293-697-1216	Sequence 1216, App	645	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
573	10.4	74.3	3264	7	US-11-217-529-3050	Sequence 3050, App	646	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
574	10.4	74.3	3276	7	US-11-217-529-2030	Sequence 2030, App	647	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
575	10.4	74.3	3287	7	US-11-217-529-78908	Sequence 78908, App	648	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
576	10.4	74.3	3420	7	US-11-217-529-71	Sequence 71, Appl	649	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
577	10.4	74.3	3424	7	US-11-293-697-663	Sequence 663, App	650	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
578	10.4	74.3	3547	7	US-11-293-697-1122	Sequence 1122, App	651	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
579	10.4	74.3	3614	7	US-11-302-678-61	Sequence 61, Appl	652	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
580	10.4	74.3	3660	7	US-11-217-529-2996	Sequence 2996, App	653	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
581	10.4	74.3	3693	7	US-11-217-529-77316	Sequence 77316, A	654	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
582	10.4	74.3	3726	7	US-11-293-697-533	Sequence 533, App	655	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
583	10.4	74.3	3813	7	US-11-217-529-3352	Sequence 3352, App	656	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
584	10.4	74.3	3822	7	US-11-293-697-877	Sequence 877, App	657	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
585	10.4	74.3	3841	7	US-11-293-697-1374	Sequence 1374, App	658	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
586	10.4	74.3	3873	7	US-11-217-529-77429	Sequence 77429, App	659	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
587	10.4	74.3	3935	7	US-11-293-697-534	Sequence 534, App	660	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
588	10.4	74.3	3985	7	US-11-255-147-7	Sequence 7, Appl	661	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
589	10.4	74.3	4068	7	US-11-217-529-48	Sequence 48, Appl	662	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
590	10.4	74.3	4122	6	US-10-505-928-427	Sequence 427, App	663	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
591	10.4	74.3	4246	6	US-10-505-928-544	Sequence 544, App	664	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
592	10.4	74.3	4314	6	US-10-511-937-553	Sequence 553, App	665	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
593	10.4	74.3	4326	7	US-11-121-154-160	Sequence 160, App	666	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
594	10.4	74.3	4498	7	US-11-217-529-190990	Sequence 190990, App	667	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
595	10.4	74.3	4637	7	US-11-301-554-804	Sequence 804, App	668	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
596	10.4	74.3	4791	6	US-10-505-928-647	Sequence 647, App	669	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
597	10.4	74.3	5072	6	US-10-953-349-7998	Sequence 7998, App	670	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
598	10.4	74.3	5310	6	US-11-217-529-77298	Sequence 77298, A	671	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
599	10.4	74.3	5650	6	US-10-505-928-212	Sequence 212, App	672	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
600	10.4	74.3	6400	6	US-10-505-928-396	Sequence 396, App	673	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
601	10.4	74.3	6438	7	US-11-217-529-173840	Sequence 173840, A	674	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
602	10.4	74.3	7463	6	US-10-953-349-58474	Sequence 58474, A	675	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
603	10.4	74.3	8019	7	US-11-217-529-76544	Sequence 76544, A	676	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
604	10.4	74.3	8764	7	US-11-322-999-137	Sequence 137, App	677	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
605	10.4	74.3	8833	6	US-10-505-928-785	Sequence 785, App	678	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
606	10.4	74.3	9246	7	US-11-217-529-3285	Sequence 3285, App	679	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
607	10.4	74.3	9973	6	US-10-857-260-29	Sequence 29, Appl	680	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
608	10.4	74.3	10211	6	US-10-505-928-326	Sequence 326, App	681	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
609	10.4	74.3	10581	7	US-11-217-529-4304	Sequence 4304, App	682	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl

c 683	10	71.4	914	6	US-10-953-349-39424	Sequence 39424, A	c 756	10	71.4	1627	7	US-11-293-697-1835	Sequence 1835, Ap
c 684	10	71.4	930	7	US-11-217-529-4685	Sequence 4685, Ap	c 757	10	71.4	1628	7	US-11-293-697-1846	Sequence 1846, Ap
c 685	10	71.4	945	7	US-11-217-529-5482	Sequence 5482, Ap	c 758	10	71.4	1630	7	US-11-293-697-1630	Sequence 1630, Ap
c 686	10	71.4	960	7	US-11-217-529-82143	Sequence 82143, A	c 759	10	71.4	1633	7	US-11-293-697-1852	Sequence 1852, Ap
c 687	10	71.4	963	7	US-11-217-529-2815	Sequence 2815, Ap	c 760	10	71.4	1633	7	US-11-293-697-2197	Sequence 2197, Ap
c 688	10	71.4	990	7	US-11-217-529-6230	Sequence 6230, Ap	c 761	10	71.4	1639	7	US-11-293-697-2238	Sequence 2238, Ap
c 689	10	71.4	1026	7	US-11-219-563-135	Sequence 135, App	c 762	10	71.4	1701	7	US-11-106-762-10	Sequence 10, Appl
c 690	10	71.4	1094	6	US-10-953-349-35709	Sequence 35709, A	c 763	10	71.4	1704	7	US-11-217-529-77224	Sequence 77224, A
c 691	10	71.4	1095	7	US-11-217-529-82043	Sequence 82043, A	c 764	10	71.4	1725	6	US-10-953-349-27632	Sequence 27632, A
c 692	10	71.4	1107	7	US-11-217-529-78001	Sequence 78001, A	c 765	10	71.4	1731	7	US-11-244-678-5	Sequence 5, Appl
c 693	10	71.4	1108	6	US-10-953-349-411	Sequence 411, App	c 766	10	71.4	1750	6	US-10-953-349-10054	Sequence 10054, A
c 694	10	71.4	1119	7	US-11-217-529-76178	Sequence 76178, A	c 767	10	71.4	1759	7	US-11-293-697-2324	Sequence 2324, Ap
c 695	10	71.4	1129	6	US-10-953-349-18277	Sequence 18277, A	c 768	10	71.4	1763	7	US-11-293-697-1840	Sequence 1840, Ap
c 696	10	71.4	1132	6	US-10-953-349-3258	Sequence 3258, Ap	c 769	10	71.4	1767	6	US-10-953-349-22189	Sequence 22189, A
c 697	10	71.4	1151	6	US-10-953-349-35098	Sequence 35098, A	c 770	10	71.4	1775	6	US-10-953-349-32421	Sequence 32421, A
c 698	10	71.4	1152	6	US-10-953-349-28455	Sequence 28455, A	c 771	10	71.4	1790	7	US-11-293-697-2345	Sequence 2345, Ap
c 699	10	71.4	1156	6	US-10-953-349-11844	Sequence 11844, A	c 772	10	71.4	1802	7	US-11-293-697-2009	Sequence 2009, Ap
c 700	10	71.4	1188	6	US-10-953-349-28881	Sequence 28881, A	c 773	10	71.4	1805	6	US-10-953-349-12895	Sequence 12895, A
c 701	10	71.4	1213	7	US-11-244-678-6	Sequence 6, Appl	c 774	10	71.4	1815	7	US-11-217-529-75749	Sequence 75749, A
c 702	10	71.4	1227	6	US-10-953-349-27530	Sequence 27530, A	c 775	10	71.4	1820	7	US-11-244-678-3	Sequence 3, Appl
c 703	10	71.4	1248	7	US-11-217-529-39	Sequence 39, Appl	c 776	10	71.4	1821	7	US-11-293-697-1804	Sequence 1804, Ap
c 704	10	71.4	1251	7	US-11-217-529-248	Sequence 248, App	c 777	10	71.4	1822	7	US-11-293-697-130	Sequence 130, App
c 705	10	71.4	1255	6	US-10-953-349-11798	Sequence 11798, A	c 778	10	71.4	1828	7	US-11-244-678-1	Sequence 1, Appl
c 706	10	71.4	1297	7	US-11-302-678-54	Sequence 54, Appl	c 779	10	71.4	1837	7	US-11-293-697-1660	Sequence 1660, Ap
c 707	10	71.4	1307	6	US-10-953-349-27753	Sequence 27753, A	c 780	10	71.4	1837	7	US-11-293-697-1870	Sequence 1870, Ap
c 708	10	71.4	1312	6	US-10-953-349-21662	Sequence 21662, A	c 781	10	71.4	1842	7	US-11-217-529-1606	Sequence 1606, Ap
c 709	10	71.4	1330	6	US-10-981-300-19	Sequence 19, Appl	c 782	10	71.4	1857	7	US-11-217-529-2428	Sequence 2428, Ap
c 710	10	71.4	1330	6	US-10-953-349-14318	Sequence 14318, A	c 783	10	71.4	1871	6	US-10-196-749-301	Sequence 301, App
c 711	10	71.4	1344	6	US-10-713-648A-51	Sequence 51, Appl	c 784	10	71.4	1871	7	US-11-101-316-91	Sequence 91, Appl
c 712	10	71.4	1350	6	US-10-953-349-31595	Sequence 31595, A	c 785	10	71.4	1897	6	US-10-953-349-19352	Sequence 19352, A
c 713	10	71.4	1360	6	US-10-953-349-31213	Sequence 31213, A	c 786	10	71.4	1904	6	US-10-505-928-546	Sequence 546, App
c 714	10	71.4	1362	6	US-10-981-300-15	Sequence 15, Appl	c 787	10	71.4	1906	7	US-11-293-697-551	Sequence 551, App
c 715	10	71.4	1362	7	US-11-217-529-77394	Sequence 77394, A	c 788	10	71.4	1941	7	US-11-293-697-2086	Sequence 2086, Ap
c 716	10	71.4	1395	7	US-11-211-917-21	Sequence 21, Appl	c 789	10	71.4	1943	6	US-10-953-349-37312	Sequence 37312, A
c 717	10	71.4	1398	7	US-11-211-917-37	Sequence 37, Appl	c 790	10	71.4	2027	6	US-10-953-349-32588	Sequence 32588, A
c 718	10	71.4	1401	7	US-11-211-917-29	Sequence 29, Appl	c 791	10	71.4	2029	6	US-10-505-928-865	Sequence 865, App
c 719	10	71.4	1401	7	US-11-211-917-69	Sequence 69, Appl	c 792	10	71.4	2059	6	US-10-511-937-507	Sequence 507, App
c 720	10	71.4	1401	7	US-11-211-917-85	Sequence 85, Appl	c 793	10	71.4	2079	7	US-11-217-529-77476	Sequence 77476, A
c 721	10	71.4	1407	7	US-11-155-444-17	Sequence 17, Appl	c 794	10	71.4	2086	7	US-11-293-697-1875	Sequence 1875, Ap
c 722	10	71.4	1410	7	US-11-211-917-53	Sequence 53, Appl	c 795	10	71.4	2094	7	US-11-155-444-1	Sequence 1, Appl
c 723	10	71.4	1413	7	US-11-211-917-61	Sequence 61, Appl	c 796	10	71.4	2106	7	US-11-155-444-7	Sequence 7, Appl
c 724	10	71.4	1416	7	US-11-211-917-77	Sequence 77, Appl	c 797	10	71.4	2118	6	US-10-953-349-35155	Sequence 35155, A
c 725	10	71.4	1416	7	US-11-211-917-5	Sequence 5, Appl	c 798	10	71.4	2128	6	US-10-196-749-171	Sequence 171, App
c 726	10	71.4	1416	7	US-11-211-917-45	Sequence 45, Appl	c 799	10	71.4	2133	7	US-11-181-115-2	Sequence 2, Appl
c 727	10	71.4	1419	6	US-10-546-594-129	Sequence 129, App	c 800	10	71.4	2133	7	US-11-181-115-39	Sequence 39, Appl
c 728	10	71.4	1420	6	US-10-953-349-12396	Sequence 12396, A	c 801	10	71.4	2139	7	US-11-217-529-75693	Sequence 75693, A
c 729	10	71.4	1425	7	US-11-211-917-13	Sequence 13, Appl	c 802	10	71.4	2170	7	US-11-293-697-1753	Sequence 1753, Ap
c 730	10	71.4	1443	7	US-11-217-529-1848	Sequence 1848, Ap	c 803	10	71.4	2187	7	US-11-217-529-4382	Sequence 4382, Ap
c 731	10	71.4	1452	6	US-10-953-349-38070	Sequence 38070, A	c 804	10	71.4	2192	6	US-10-953-349-14231	Sequence 14231, A
c 732	10	71.4	1455	7	US-11-217-529-1502	Sequence 1502, Ap	c 805	10	71.4	2214	6	US-11-293-697-2000	Sequence 2000, Ap
c 733	10	71.4	1455	7	US-11-217-529-77427	Sequence 77427, A	c 806	10	71.4	2225	7	US-11-293-697-916	Sequence 916, App
c 734	10	71.4	1458	6	US-10-953-349-24219	Sequence 24219, A	c 807	10	71.4	2229	7	US-11-293-697-1081	Sequence 1081, Ap
c 735	10	71.4	1473	6	US-10-953-349-24770	Sequence 24770, A	c 808	10	71.4	2251	7	US-11-293-697-184	Sequence 184, App
c 736	10	71.4	1484	1	US-09-949-925-54	Sequence 54, Appl	c 809	10	71.4	2290	7	US-11-293-697-1793	Sequence 1793, Ap
c 737	10	71.4	1518	7	US-11-217-529-3186	Sequence 3186, Ap	c 810	10	71.4	2301	7	US-11-217-529-76159	Sequence 76159, A
c 738	10	71.4	1520	6	US-10-953-349-5515	Sequence 5515, Ap	c 811	10	71.4	2315	6	US-10-953-349-31228	Sequence 31228, A
c 739	10	71.4	1542	6	US-10-953-349-336	Sequence 336, App	c 812	10	71.4	2391	7	US-11-217-529-82497	Sequence 82497, A
c 740	10	71.4	1557	7	US-11-302-678-52	Sequence 52, Appl	c 813	10	71.4	2411	7	US-11-293-697-994	Sequence 994, App
c 741	10	71.4	1566	7	US-11-293-697-1850	Sequence 1850, Ap	c 814	10	71.4	2430	7	US-11-217-529-1342	Sequence 1342, Ap
c 742	10	71.4	1575	6	US-10-953-349-21291	Sequence 21291, A	c 815	10	71.4	2476	7	US-11-293-697-110	Sequence 110, App
c 743	10	71.4	1578	7	US-11-219-563-131	Sequence 131, App	c 816	10	71.4	2530	7	US-11-066-633-1	Sequence 1, Appl
c 744	10	71.4	1590	6	US-10-505-928-838	Sequence 838, Appl	c 817	10	71.4	2574	7	US-11-293-697-2437	Sequence 2437, Ap
c 745	10	71.4	1590	7	US-11-106-014-43	Sequence 43, Appl	c 818	10	71.4	2627	7	US-11-293-697-1527	Sequence 1527, Ap
c 746	10	71.4	1602	7	US-11-293-697-1849	Sequence 1849, Ap	c 819	10	71.4	2627	7	US-11-293-697-1663	Sequence 1663, Ap
c 747	10	71.4	1605	7	US-11-293-697-1842	Sequence 1842, Ap	c 820	10	71.4	2752	7	US-11-293-697-2385	Sequence 2385, Ap
c 748	10	71.4	1612	7	US-11-293-697-1803	Sequence 1803, Ap	c 821	10	71.4	2769	6	US-10-953-349-11407	Sequence 11407, A
c 749	10	71.4	1613	7	US-11-293-697-1839	Sequence 1839, Ap	c 822	10	71.4	2770	7	US-11-293-697-1700	Sequence 1700, Ap
c 750	10	71.4	1613	7	US-11-293-697-1841	Sequence 1841, Ap	c 823	10	71.4	2795	7	US-11-293-697-1621	Sequence 1621, Ap
c 751	10	71.4	1618	7	US-11-293-697-1848	Sequence 1848, Ap	c 824	10	71.4	2840	6	US-10-953-349-34238	Sequence 34238, A
c 752	10	71.4	1618	7	US-11-293-697-1845	Sequence 1845, Ap	c 825	10	71.4	2859	7	US-11-293-697-1056	Sequence 1056, Ap
c 753	10	71.4	1620	7	US-11-293-697-1851	Sequence 1851, Ap	c 826	10	71.4	2898	7	US-11-217-529-1716	Sequence 1716, Ap
c 754	10	71.4	1622	7	US-11-293-697-1844	Sequence 1844, Ap	c 827	10	71.4	2952	7	US-11-293-697-1728	Sequence 1728, Ap
c 755	10	71.4	1624	7	US-11-293-697-1748	Sequence 1748, Ap	c 828	10	71.4	3047	6	US-10-953-349-11451	Sequence 11451, A

C 829	10	71.4	3158	7	US-11-293-697-1741	Sequence 1741, Ap	902	9.8	70.0	25	7	US-11-217-529-98861	Sequence 98861, A
C 830	10	71.4	3201	6	US-10-370-959-3	Sequence 3, Appli	903	9.8	70.0	25	7	US-11-217-529-98868	Sequence 98868, A
C 831	10	71.4	3201	7	US-11-302-678-51	Sequence 51, Appl	904	9.8	70.0	25	7	US-11-217-529-98869	Sequence 98869, A
C 832	10	71.4	3265	7	US-11-293-697-1409	Sequence 1409, Ap	906	9.8	70.0	25	7	US-11-217-529-100564	Sequence 100564, A
C 833	10	71.4	3302	7	US-11-293-697-1167	Sequence 1167, Ap	906	9.8	70.0	25	7	US-11-217-529-108491	Sequence 108491, A
C 834	10	71.4	3512	7	US-11-293-697-501	Sequence 501, Appl	907	9.8	70.0	25	7	US-11-217-529-123901	Sequence 123901, A
C 835	10	71.4	3637	6	US-10-370-959-1	Sequence 1, Appli	908	9.8	70.0	25	7	US-11-217-529-125016	Sequence 125016, A
C 836	10	71.4	3637	7	US-11-302-678-49	Sequence 49, Appl	909	9.8	70.0	25	7	US-11-217-529-125019	Sequence 125019, A
C 837	10	71.4	3693	7	US-11-217-529-78150	Sequence 78150, A	910	9.8	70.0	25	7	US-11-217-529-130122	Sequence 130122, A
C 838	10	71.4	3759	6	US-10-473-173-12	Sequence 12, Appl	911	9.8	70.0	25	7	US-11-217-529-138709	Sequence 138709, A
C 839	10	71.4	4077	7	US-11-217-529-76732	Sequence 76732, A	912	9.8	70.0	25	7	US-11-217-529-140211	Sequence 140211, A
C 840	10	71.4	4086	7	US-11-301-554-1801	Sequence 1803, Ap	913	9.8	70.0	25	7	US-11-217-529-145421	Sequence 145421, A
C 841	10	71.4	4118	6	US-11-223-738-4	Sequence 4, Appli	914	9.8	70.0	25	7	US-11-217-529-151303	Sequence 151303, A
C 842	10	71.4	4446	6	US-10-511-937-2840	Sequence 2840, Ap	915	9.8	70.0	25	7	US-11-217-529-153607	Sequence 153607, A
C 843	10	71.4	4712	6	US-10-505-928-164	Sequence 164, App	916	9.8	70.0	25	7	US-11-217-529-169927	Sequence 169927, A
C 844	10	71.4	4791	6	US-10-505-928-647	Sequence 647, App	917	9.8	70.0	25	7	US-11-217-529-171931	Sequence 171931, A
C 845	10	71.4	4941	6	US-10-713-648A-34	Sequence 34, Appl	918	9.8	70.0	25	7	US-11-217-529-171936	Sequence 171936, A
C 846	10	71.4	5193	7	US-11-270-040-5	Sequence 5, Appli	919	9.8	70.0	25	7	US-11-217-529-176914	Sequence 176914, A
C 847	10	71.4	5479	6	US-10-505-928-472	Sequence 472, App	920	9.8	70.0	25	7	US-11-217-529-182432	Sequence 182432, A
C 848	10	71.4	5862	6	US-10-505-928-25	Sequence 25, Appl	921	9.8	70.0	25	7	US-11-217-529-193608	Sequence 193608, A
C 849	10	71.4	5994	6	US-10-505-928-701	Sequence 701, App	922	9.8	70.0	25	7	US-11-217-529-193610	Sequence 193610, A
C 850	10	71.4	6152	6	US-10-528-659-6	Sequence 6, Appli	923	9.8	70.0	25	7	US-11-217-529-195571	Sequence 195571, A
C 851	10	71.4	6188	7	US-11-301-554-1823	Sequence 1823, Ap	924	9.8	70.0	28	6	US-11-303-896-7	Sequence 7, Appli
C 852	10	71.4	6253	6	US-10-505-928-328	Sequence 328, App	925	9.8	70.0	50	6	US-10-511-937-2691	Sequence 2691, Ap
C 853	10	71.4	6928	6	US-10-505-928-781	Sequence 781, App	926	9.8	70.0	51	7	US-11-143-642-825	Sequence 825, App
C 854	10	71.4	7103	7	US-11-226-605-87	Sequence 87, Appl	927	9.8	70.0	51	7	US-11-143-642-1805	Sequence 1805, Ap
C 855	10	71.4	7680	6	US-10-505-928-635	Sequence 635, App	928	9.8	70.0	51	7	US-11-245-248-1125	Sequence 1125, Ap
C 856	10	71.4	7680	6	US-10-505-928-858	Sequence 858, App	929	9.8	70.0	51	7	US-11-245-248-1250	Sequence 1250, Ap
C 857	10	71.4	8540	7	US-11-183-218-57	Sequence 57, Appl	930	9.8	70.0	66	7	US-11-267-871-424	Sequence 424, App
C 858	10	71.4	8687	7	US-11-297-317-15	Sequence 15, Appl	931	9.8	70.0	66	7	US-11-267-871-424	Sequence 424, App
C 859	10	71.4	8687	7	US-11-297-317-16	Sequence 16, Appl	932	9.8	70.0	81	7	US-11-194-055-105	Sequence 105, App
C 860	10	71.4	9209	7	US-11-183-218-58	Sequence 58, Appl	933	9.8	70.0	99	7	US-11-217-529-174159	Sequence 174159, A
C 861	10	71.4	9426	7	US-11-217-529-1662	Sequence 1662, Ap	935	9.8	70.0	108	7	US-11-194-055-32	Sequence 32, Appl
C 862	10	71.4	9685	7	US-11-226-605-88	Sequence 88, Appl	936	9.8	70.0	144	7	US-11-217-529-3921	Sequence 3921, Ap
C 863	10	71.4	9730	6	US-10-501-834-219	Sequence 219, App	937	9.8	70.0	150	7	US-11-252-276-137	Sequence 137, Appl
C 864	10	71.4	9780	7	US-11-187-863-1	Sequence 1, Appli	937	9.8	70.0	160	1	US-09-728-720A-3	Sequence 3, Appli
C 865	10	71.4	22118	7	US-11-284-877-16	Sequence 16, Appl	938	9.8	70.0	162	7	US-11-217-529-76783	Sequence 76783, A
C 866	10	71.4	394191	6	US-10-506-549-3	Sequence 3, Appli	939	9.8	70.0	180	7	US-11-217-529-4687	Sequence 4687, Ap
C 867	9.8	70.0	25	7	US-11-217-529-6687	Sequence 6687, Ap	940	9.8	70.0	194	7	US-11-301-554-1443	Sequence 1443, Ap
C 868	9.8	70.0	25	7	US-11-217-529-9275	Sequence 9275, Ap	941	9.8	70.0	198	6	US-10-468-193-4	Sequence 4, Appli
C 869	9.8	70.0	25	7	US-11-217-529-10179	Sequence 10179, A	942	9.8	70.0	204	7	US-11-217-529-166752	Sequence 166752, A
C 870	9.8	70.0	25	7	US-11-217-529-10209	Sequence 10209, A	943	9.8	70.0	219	7	US-11-217-529-166934	Sequence 166934, A
C 871	9.8	70.0	25	7	US-11-217-529-11970	Sequence 11970, A	944	9.8	70.0	231	7	US-11-217-529-80468	Sequence 80468, A
C 872	9.8	70.0	25	7	US-11-217-529-22251	Sequence 22251, A	945	9.8	70.0	257	6	US-10-488-619-210	Sequence 210, App
C 873	9.8	70.0	25	7	US-11-217-529-39253	Sequence 39253, A	946	9.8	70.0	262	6	US-10-488-619-696	Sequence 696, App
C 874	9.8	70.0	25	7	US-11-217-529-39927	Sequence 39927, A	947	9.8	70.0	273	7	US-11-217-529-166753	Sequence 166753, A
C 875	9.8	70.0	25	7	US-11-217-529-42071	Sequence 42071, A	948	9.8	70.0	291	7	US-11-301-554-832	Sequence 832, App
C 876	9.8	70.0	25	7	US-11-217-529-46063	Sequence 46063, A	949	9.8	70.0	309	7	US-11-217-529-75967	Sequence 75967, A
C 877	9.8	70.0	25	7	US-11-217-529-47739	Sequence 47739, A	950	9.8	70.0	325	7	US-11-301-554-448	Sequence 448, App
C 878	9.8	70.0	25	7	US-11-217-529-47740	Sequence 47740, A	951	9.8	70.0	327	7	US-11-246-999-109	Sequence 109, App
C 879	9.8	70.0	25	7	US-11-217-529-48233	Sequence 48233, A	952	9.8	70.0	348	7	US-11-217-529-5998	Sequence 5998, Ap
C 880	9.8	70.0	25	7	US-11-217-529-48530	Sequence 48530, A	953	9.8	70.0	351	7	US-11-217-529-75341	Sequence 75341, A
C 881	9.8	70.0	25	7	US-11-217-529-49413	Sequence 49413, A	954	9.8	70.0	354	7	US-11-217-529-190952	Sequence 190952, A
C 882	9.8	70.0	25	7	US-11-217-529-49414	Sequence 49414, A	955	9.8	70.0	366	7	US-11-217-529-76019	Sequence 76019, A
C 883	9.8	70.0	25	7	US-11-217-529-49417	Sequence 49417, A	956	9.8	70.0	378	7	US-11-217-529-173336	Sequence 173336, A
C 884	9.8	70.0	25	7	US-11-217-529-49423	Sequence 49423, A	957	9.8	70.0	385	7	US-11-301-554-1337	Sequence 1337, Ap
C 885	9.8	70.0	25	7	US-11-217-529-58045	Sequence 58045, A	958	9.8	70.0	393	7	US-11-322-999-107	Sequence 107, App
C 886	9.8	70.0	25	7	US-11-217-529-58048	Sequence 58048, A	959	9.8	70.0	399	7	US-11-217-529-166939	Sequence 166939, A
C 887	9.8	70.0	25	7	US-11-217-529-58113	Sequence 58113, A	960	9.8	70.0	403	6	US-10-488-619-2050	Sequence 2050, Ap
C 888	9.8	70.0	25	7	US-11-217-529-58840	Sequence 58840, A	961	9.8	70.0	408	7	US-11-217-529-82767	Sequence 82767, A
C 889	9.8	70.0	25	7	US-11-217-529-60985	Sequence 60985, A	962	9.8	70.0	415	6	US-10-488-619-2051	Sequence 2051, Ap
C 890	9.8	70.0	25	7	US-11-217-529-61248	Sequence 61248, A	963	9.8	70.0	420	6	US-10-488-619-1634	Sequence 1634, Ap
C 891	9.8	70.0	25	7	US-11-217-529-62417	Sequence 62417, A	964	9.8	70.0	421	6	US-10-488-619-206	Sequence 206, App
C 892	9.8	70.0	25	7	US-11-217-529-64001	Sequence 64001, A	965	9.8	70.0	426	7	US-11-301-554-459	Sequence 459, App
C 893	9.8	70.0	25	7	US-11-217-529-69733	Sequence 69733, A	966	9.8	70.0	426	7	US-11-301-554-459	Sequence 459, App
C 894	9.8	70.0	25	7	US-11-217-529-72681	Sequence 72681, A	967	9.8	70.0	435	6	US-11-217-529-265	Sequence 265, App
C 895	9.8	70.0	25	7	US-11-217-529-72906	Sequence 72906, A	968	9.8	70.0	439	6	US-10-488-619-2479	Sequence 2479, Ap
C 896	9.8	70.0	25	7	US-11-217-529-82839	Sequence 82839, A	969	9.8	70.0	444	6	US-10-488-619-1101	Sequence 1101, Ap
C 897	9.8	70.0	25	7	US-11-217-529-86216	Sequence 86216, A	970	9.8	70.0	453	7	US-11-217-529-82691	Sequence 82691, A
C 898	9.8	70.0	25	7	US-11-217-529-88761	Sequence 88761, A	971	9.8	70.0	454	6	US-10-488-619-2372	Sequence 2372, Ap
C 899	9.8	70.0	25	7	US-11-217-529-98850	Sequence 98850, A	972	9.8	70.0	458	6	US-10-488-619-915	Sequence 915, App
C 900	9.8	70.0	25	7	US-11-217-529-98856	Sequence 98856, A	973	9.8	70.0	463	6	US-10-953-349-30917	Sequence 30917, A
C 901	9.8	70.0	25	7	US-11-217-529-98857	Sequence 98857, A	974	9.8	70.0	464	6	US-10-488-619-2480	Sequence 2480, Ap

c 975 9.8 70.0 473 6 US-10-488-619-2659 Sequence 2659, Ap
c 976 9.8 70.0 480 6 US-10-488-619-2373 Sequence 2373, Ap
c 977 9.8 70.0 480 7 US-11-248-986-1 Sequence 1, Appl
c 978 9.8 70.0 483 6 US-10-488-619-298 Sequence 298, App
c 979 9.8 70.0 493 7 US-11-301-554-193 Sequence 193, App
c 980 9.8 70.0 495 7 US-11-217-529-79338 Sequence 79338, A
c 981 9.8 70.0 504 6 US-10-488-619-1248 Sequence 1248, Ap
c 982 9.8 70.0 507 6 US-11-217-529-4975 Sequence 4975, Ap
c 983 9.8 70.0 507 7 US-11-217-529-80087 Sequence 80087, A
c 984 9.8 70.0 525 7 US-11-217-529-844 Sequence 844, App
c 985 9.8 70.0 534 7 US-11-301-554-844 Sequence 844, App
c 986 9.8 70.0 534 7 US-11-217-529-81103 Sequence 81103, A
c 987 9.8 70.0 541 6 US-10-953-349-36788 Sequence 36788, A
c 988 9.8 70.0 546 7 US-11-301-554-129 Sequence 129, App
c 989 9.8 70.0 553 6 US-10-511-937-2808 Sequence 2808, Ap
c 990 9.8 70.0 559 6 US-10-473-173-341 Sequence 341, App
c 991 9.8 70.0 561 6 US-10-488-619-822 Sequence 822, App
c 992 9.8 70.0 568 6 US-10-488-619-1026 Sequence 1026, Ap
c 993 9.8 70.0 569 6 US-10-488-619-2716 Sequence 2716, Ap
c 994 9.8 70.0 570 6 US-10-473-173-19 Sequence 19, Appl
c 995 9.8 70.0 571 6 US-10-488-619-2657 Sequence 2657, Ap
c 996 9.8 70.0 574 6 US-10-488-619-2655 Sequence 2655, Ap
c 997 9.8 70.0 574 6 US-10-953-349-6017 Sequence 6017, Ap
c 998 9.8 70.0 576 6 US-10-488-619-2401 Sequence 2401, Ap
c 999 9.8 70.0 576 7 US-11-217-529-82432 Sequence 82432, A
1000 9.8 70.0 581 6 US-10-488-619-2947 Sequence 2947, Ap

ALIGNMENTS

RESULT 1
US-10-511-937-2635/c
; Sequence 2635, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2635
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2635

Query Match 88.6%; Score 12.4; DB 6; Length 50;
Best Local Similarity 92.9%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 19 GAAGGGTGTGCTTAC 6

RESULT 2

US-11-217-529-77707/c
; Sequence 77707, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77707
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77707

Query Match 88.6%; Score 12.4; DB 7; Length 765;
Best Local Similarity 92.9%; Pred. No. 48;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 335 GAAGTTGTGCTTAC 322

RESULT 3
US-10-953-349-20394
; Sequence 20394, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCED-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20394
; LENGTH: 1019
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20394

Query Match 88.6%; Score 12.4; DB 6; Length 1019;
Best Local Similarity 92.9%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 566 GAAGGTGTGCTCAC 579

RESULT 4
US-11-217-529-3002
; Sequence 3002, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS


```
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3002
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3002

Query Match      88.6%; Score 12.4; DB 7; Length 1161;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
      |||||
Db      457 GAAGGTGTGCTAAC 470

RESULT 5
US-10-953-349-8649
; Sequence 8649, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8649
; LENGTH: 1304
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8649

Query Match      88.6%; Score 12.4; DB 6; Length 1304;
Best Local Similarity 92.9%; Pred. No. 53;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
      |||||
Db      712 GAAGGTGTGCTTAC 725

RESULT 6
US-10-511-937-2804/c
; Sequence 2804, Application US/10511937
; Publication No. US20060088936A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
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; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2804
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2804

Query Match      88.6%; Score 12.4; DB 6; Length 1451;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
      |||||
Db      1270 GAAGGGGTGCTTAC 1257

RESULT 7
US-11-217-529-82278
; Sequence 82278, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82278
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82278

Query Match      88.6%; Score 12.4; DB 7; Length 2079;
Best Local Similarity 92.9%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
      |||||
Db      489 GAAGGTGAGCTTAC 502

RESULT 8
US-10-953-349-4556/c
; Sequence 4556, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4556
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4556

Query Match      88.6%; Score 12.4; DB 6; Length 3435;
Best Local Similarity 92.9%; Pred. No. 64;
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 2396 GAAGGTGTGCTTCC 2383

RESULT 9

US-10-505-928-151/c

; Sequence 151, Application US/10505928

; Publication No. US2006008532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 151

; LENGTH: 128361

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-505-928-151

Query Match

Best Local Similarity 88.6%; Score 12.4; DB 6; Length 128361;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 55351 GAAGTGGGCTTAC 55338

RESULT 10

US-10-953-349-23971

; Sequence 23971, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 23971

; LENGTH: 650

; TYPE: DNA

; ORGANISM: Glycine max

US-10-953-349-23971

Query Match

Best Local Similarity 85.7%; Score 12; DB 6; Length 650;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12

|||||

Db 311 GAAGGTGTGCTT 322

RESULT 11

US-10-953-349-12654

; Sequence 12654, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 12654

; LENGTH: 651

; TYPE: DNA

; ORGANISM: Glycine max

US-10-953-349-12654

Query Match

Best Local Similarity 85.7%; Score 12; DB 6; Length 651;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12

|||||

Db 311 GAAGGTGTGCTT 322

RESULT 12

US-11-217-529-2897

; Sequence 2897, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUDIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2897

; LENGTH: 951

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-11-217-529-2897

Query Match

Best Local Similarity 85.7%; Score 12; DB 7; Length 951;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTA 13

|||||

Db 719 AAGGTGTGCTTA 730

RESULT 13

US-10-953-349-17567

; Sequence 17567, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 17567

; LENGTH: 1212

; TYPE: DNA

; ORGANISM: Glycine max

US-10-953-349-17567

Query Match

Best Local Similarity 85.7%; Score 12; DB 6; Length 1212;

Best Local Similarity 100.0%; Pred. No. 93;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 109 GAAGGTGTGCTT 120

RESULT 14

US-11-024-544A-17/c
; Sequence 17, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (466)..(466)
; OTHER INFORMATION: n is a, c, g, or t
US-11-024-544A-17

Query Match 85.7%; Score 12; DB 7; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 135 GAAGGTGTGCTT 124

RESULT 15

US-11-190-750-131/c
; Sequence 131, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (466)..(466)
; OTHER INFORMATION: n is a, c, g, or t
US-11-190-750-131

Query Match 85.7%; Score 12; DB 7; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 135 GAAGGTGTGCTT 124

RESULT 16

US-11-264-784-83/c
; Sequence 83, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: DGAT1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (466)..(466)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-784-83

Query Match 85.7%; Score 12; DB 7; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 135 GAAGGTGTGCTT 124

RESULT 17

US-11-264-737-124/c
; Sequence 124, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: DCOSEXHAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124

```
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: DGAT1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (466)..(466)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-737-124

Query Match      85.7%; Score 12; DB 7; Length 1578;
Best Local Similarity 100.0%; Pred.No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
Db 135 GAAGGTGTGCTT 124

RESULT 18
US-11-217-529-81407/c
; Sequence 81407, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIOHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81407
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81407

Query Match      85.7%; Score 12; DB 7; Length 1584;
Best Local Similarity 100.0%; Pred.No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
Db 1154 GAAGGTGTGCTT 1143

RESULT 19
US-10-953-349-12369
; Sequence 12369, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12369
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (607)..(607)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (661)..(661)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (681)..(681)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (698)..(698)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (769)..(769)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (784)..(784)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (801)..(801)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (805)..(805)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (826)..(826)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (843)..(843)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (871)..(871)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (887)..(887)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (912)..(912)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (962)..(962)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (964)..(964)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (980)..(980)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1012)..(1012)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12369
```

Query Match 85.7%; Score 12; DB 6; Length 1667;
Best Local Similarity 100.0%; Pred.No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 1042 GAAGGTGTGCTT 1053

RESULT 20

US-11-024-544A-156/c
; Sequence 156, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 156
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1093)..(1093)
; OTHER INFORMATION: n is a, c, g, or t
US-11-024-544A-156

Query Match 85.7%; Score 12; DB 7; Length 1683;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 367 GAAGGTGTGCTT 356

RESULT 21

US-11-190-750-127/c
; Sequence 127, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 127
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1093)..(1093)
; OTHER INFORMATION: n is a, c, g, or t
US-11-190-750-127

Query Match 85.7%; Score 12; DB 7; Length 1683;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||

Db 367 GAAGGTGTGCTT 356

RESULT 22

US-10-953-349-16812
; Sequence 16812, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16812
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-16812

Query Match 85.7%; Score 12; DB 6; Length 1749;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 673 GAAGGTGTGCTT 684

RESULT 23

US-11-145-307A-163/c
; Sequence 163, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Acturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-163

Query Match 85.7%; Score 12; DB 7; Length 1841;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGTGTGCTTAC 14
|||||
Db 1656 AGGTGTGCTTAC 1645

RESULT 24

US-11-217-529-2644/c
; Sequence 2644, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

```
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2644
; LENGTH: 3915
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (73)..(122)
; OTHER INFORMATION: a, c, g, t, unknown, or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1668)..(1721)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-2644

Query Match      85.7%; Score 12; DB 7; Length 3915;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY      1 GAAGGTGTGCTT 12
        |||||
Db       1634 GAAGGTGTGCTT 1623

RESULT 25
US-11-024-544A-165/c
; Sequence 165, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 165
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pMDGAT1-17
; NAME/KEY: misc_feature
; LOCATION: (467)..(467)
; OTHER INFORMATION: n is a, c, g, or t
US-11-024-544A-165

Query Match      85.7%; Score 12; DB 7; Length 8666;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY      1 GAAGGTGTGCTT 12
        |||||
Db       136 GAAGGTGTGCTT 125

RESULT 26
US-11-264-784-141/c
; Sequence 141, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
```

```
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pMDGAT1-17
; NAME/KEY: misc_feature
; LOCATION: (467)..(467)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-784-141

Query Match      85.7%; Score 12; DB 7; Length 8666;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY      1 GAAGGTGTGCTT 12
        |||||
Db       136 GAAGGTGTGCTT 125

RESULT 27
US-11-264-737-193/c
; Sequence 193, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: DOCOSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 193
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pMDGAT1-17
; NAME/KEY: misc_feature
; LOCATION: (467)..(467)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-737-193

Query Match      85.7%; Score 12; DB 7; Length 8666;
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```
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;

QY 1 GAAGGTGCTT 12
Db 136 GAAGGTGCTT 125

RESULT 28
US-11-217-529-21396/c
; Sequence 21396, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21396
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-21396

Query Match 81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGCTTAC 14
Db 22 AAGGGTGCTTAC 10

RESULT 29
US-11-217-529-21401/c
; Sequence 21401, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21401
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-21401

Query Match 81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGCTTAC 14
Db 22 AAGGGTGCTTAC 14

RESULT 30
US-11-217-529-68345
; Sequence 68345, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68345
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-68345

Query Match 81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGCTTAC 14
Db 8 AAGGTGCTATAC 20

RESULT 31
US-11-217-529-109203/c
; Sequence 109203, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 109203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-109203

Query Match 81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTA 13
Db 13 GAAGGTGCTTA 1

RESULT 32
US-11-217-529-134611/c
```

```
; Sequence 134611, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 134611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-134611

Query Match      81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
Db      21 AAGGTGTGCATAC 9
|||||

RESULT 33
US-11-217-529-1402/c
; Sequence 1402, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1402
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1402

Query Match      81.4%; Score 11.4; DB 7; Length 357;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
Db      101 AAGGGGTGCTTAC 89
|||||

RESULT 34
US-11-217-529-5611
; Sequence 5611, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
```

```
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5611
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5611

Query Match      81.4%; Score 11.4; DB 7; Length 393;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
Db      155 AAGGTGTGCATAC 167
|||||

RESULT 35
US-11-217-529-79973/c
; Sequence 79973, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79973
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79973

Query Match      81.4%; Score 11.4; DB 7; Length 429;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
Db      290 AAGGTGTGCATAC 278
|||||

RESULT 36
US-10-488-619-1258/c
; Sequence 1258, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
```


; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1258
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1258

Query Match 81.4%; Score 11.4; DB 6; Length 436;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
||| ||||| |||||
Db 115 GAGGTTGTGCTTA 103

RESULT 37
US-10-488-619-102/c
; Sequence 102, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(442)
; OTHER INFORMATION: n is g, c, a or t

US-10-488-619-102
Query Match 81.4%; Score 11.4; DB 6; Length 442;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAAGGTGTGCTTA 13
||| ||||| |||||
Db 74 GAAGGTGTGCATA 62
RESULT 38
US-10-488-619-215/c
; Sequence 215, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-215
Query Match 81.4%; Score 11.4; DB 6; Length 491;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAAGGTGTGCTTA 13
||| ||||| |||||

Db 426 GAAGGTGAGCTTA 414

RESULT 39
US-10-488-619-637/c
; Sequence 637, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 637
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-637

Query Match 81.4%; Score 11.4; DB 6; Length 513;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
||| ||||| |||||
Db 472 AAAGTGTGCTTAC 460

RESULT 40
US-10-488-619-214
; Sequence 214, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-214
Query Match 81.4%; Score 11.4; DB 6; Length 517;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
||| ||||| |||||
Db 94 GAAGGTGAGCTTA 106

RESULT 41
US-10-953-349-6188/c
; Sequence 6188, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6188

```
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6188

Query Match      81.4%; Score 11.4; DB 6; Length 538;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAAGGTGTGCTTA 13
Db      351 GAAGTTGTGCTTA 339

RESULT 42
US-10-488-619-636
; Sequence 636, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 636
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-636

Query Match      81.4%; Score 11.4; DB 6; Length 545;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGGTGTGCTTAC 14
Db      136 AAGTGTGCTTAC 148

RESULT 43
US-10-488-619-202
; Sequence 202, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-202

Query Match      81.4%; Score 11.4; DB 6; Length 547;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAAGGTGTGCTTA 13
Db      109 GAAGGTGAGCTTA 121

RESULT 44
US-10-488-619-2061
; Sequence 2061, Application US/10488619
```

```
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2061
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2061

Query Match      81.4%; Score 11.4; DB 6; Length 561;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGGTGTGCTTAC 14
Db      190 AAGCTGTGCTTAC 202

RESULT 45
US-10-488-619-1924/c
; Sequence 1924, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1924
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1924

Query Match      81.4%; Score 11.4; DB 6; Length 592;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAAGGTGTGCTTA 13
Db      531 GAAGGAGTGCTTA 519

RESULT 46
US-11-217-529-2
; Sequence 2, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
```

```
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Saccharomyces sp.
US-11-217-529-2

Query Match      81.4%; Score 11.4; DB 7; Length 609;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
   |||||
Db 451 GAAGGTGTGATTA 463

RESULT 47
US-11-217-529-1593
; Sequence 1593, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SONTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1593
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1593

Query Match      81.4%; Score 11.4; DB 7; Length 609;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
   |||||
Db 451 GAAGGTGTGATTA 463

RESULT 48
US-10-488-619-2060/c
; Sequence 2060, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2060
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2060

Query Match      81.4%; Score 11.4; DB 6; Length 668;
Best Local Similarity 92.3%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
   ||| |||||
```

```
Db 505 AAGCTGTGCTTAC 493

RESULT 49
US-10-488-619-1923
; Sequence 1923, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1923
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1923

Query Match      81.4%; Score 11.4; DB 6; Length 711;
Best Local Similarity 92.3%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
   |||||
Db 170 GAAGGAGTGCTTA 182

RESULT 50
US-11-249-111-37/c
; Sequence 37, Application US/11249111
; Publication No. US20060099623A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus
; FILE REFERENCE: 13353.1048ulc2
; CURRENT APPLICATION NUMBER: US/11/249,111
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: 10/288,930
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/148,801
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-11-249-111-37

Query Match      81.4%; Score 11.4; DB 7; Length 840;
Best Local Similarity 92.3%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
   |||||
Db 632 AAGGTGTCTTAC 620

Search completed: May 31, 2006, 22:07:44
Job time : 67 secs
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 46.9259 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-20
Perfect score: 21
Sequence: 1 tttctttttcttattaatg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

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Minimum DB seq length: 0

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Maximum Match 100%
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- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCUTUS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	100.0	36	3	US-09-109-329-14
C 2	21	100.0	36	3	US-09-109-329-15
C 3	21	100.0	59	3	US-09-109-329-3
C 4	21	100.0	89	3	US-09-109-329-4
C 5	21	100.0	108	3	US-09-109-329-13
C 6	21	100.0	2007	2	US-08-743-637B-169
C 7	21	100.0	2007	3	US-08-526-840B-169
C 8	21	100.0	2028	3	US-09-134-001C-1710
C 9	19.4	92.4	781	4	US-09-297-648-4022
C 10	19.4	92.4	6254	3	US-08-956-171E-404
C 11	19.4	92.4	6254	3	US-08-781-986A-404
C 12	19.4	92.4	23174	3	US-09-949-016-182942
C 13	19.4	92.4	23187	3	US-09-949-016-182943
C 14	18.4	87.6	459	3	US-09-328-352-1787
C 15	18.4	87.6	589	3	US-09-949-016-182944
C 16	18.4	87.6	601	3	US-09-949-016-182941
C 17	18.4	87.6	601	3	US-09-949-016-182942
C 18	18.4	87.6	601	3	US-09-949-016-182943
C 19	18.4	87.6	3650	3	US-09-710-275-3756
C 20	18.4	87.6	41737	3	US-09-949-016-182944
C 21	18.4	87.6	41741	3	US-09-949-016-16983
C 22	18.4	87.6	80269	3	US-09-949-016-16983
C 23	18.4	87.6	385136	3	US-09-949-016-16073

24	17.8	84.8	192	3	US-09-248-796A-9636	Sequence 9636, Ap
25	17.8	84.8	503	3	US-09-621-976-2887	Sequence 2887, Ap
c 26	17.8	84.8	1341	3	US-09-830-230A-572	Sequence 572, App
27	17.8	84.8	1350	7	US-08-244-205-1	Sequence 1, Appli
28	17.8	84.8	1350	7	PCT-US92-10284-1	Sequence 1, Appli
c 29	17.8	84.8	1410	3	US-09-830-230A-571	Sequence 571, App
c 30	17.8	84.8	1761	3	US-09-369-247-21	Sequence 21, Appl
c 31	17.8	84.8	1761	3	US-10-062-548-21	Sequence 21, Appl
c 32	17.8	84.8	114139	3	US-09-949-016-16536	Sequence 16536, A
c 33	17.8	84.8	173992	3	US-09-949-016-13379	Sequence 13379, A
c 34	17.8	84.8	174170	3	US-09-949-016-14810	Sequence 14810, A
c 35	17.8	84.8	174170	3	US-09-949-016-14811	Sequence 14811, A
c 36	17.8	84.8	174318	3	US-09-949-016-11880	Sequence 11880, A
c 37	17.8	84.8	174318	3	US-09-949-016-14812	Sequence 14812, A
c 38	17.8	84.8	174318	3	US-09-949-016-14813	Sequence 14813, A
c 39	17.8	84.8	256287	3	US-09-949-016-14608	Sequence 14608, A
c 40	17.8	84.8	321022	3	US-09-949-016-11852	Sequence 11852, A
c 41	17.8	84.8	321022	3	US-09-949-016-14166	Sequence 14166, A
c 42	17.4	82.9	232	3	US-09-621-976-17701	Sequence 17701, A
c 43	17.4	82.9	450	3	US-09-621-976-15099	Sequence 15099, A
c 44	17.4	82.9	601	3	US-09-949-016-27126	Sequence 27126, A
c 45	17.4	82.9	601	3	US-09-949-016-45118	Sequence 45118, A

ALIGNMENTS

RESULT 1

US-09-109-329-14/c
; Sequence 14, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-14

Query Match 100.0%; Score 21; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 72;

Mismatches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATG 21

DB 24 TTTCTTTTCTCTATTATG 4

RESULT 2

US-09-109-329-15/c
; Sequence 15, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-15

Query Match      100.0%; Score 21; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTAAATG 21
Db 24 TTTTCTTTTCTCTATTAAATG 4

RESULT 3
US-09-109-329-3/c
; Sequence 3, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-3

Query Match      100.0%; Score 21; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTAAATG 21
Db 29 TTTTCTTTTCTCTATTAAATG 9

RESULT 4
US-09-109-329-4
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
```

```
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-4

Query Match      100.0%; Score 21; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTAAATG 21
Db 43 TTTTCTTTTCTCTATTAAATG 63

RESULT 5
US-09-109-329-13/c
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-13

Query Match      100.0%; Score 21; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTAAATG 21
Db 49 TTTTCTTTTCTCTATTAAATG 29

RESULT 6
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-743-637B-169

Query Match 100.0%; Score 21; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAAATG 21
Db 955 TTTCTTTTCTCTATTAAATG 935

RESULT 7
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-526-840B-169

Query Match 100.0%; Score 21; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAAATG 21
Db 955 TTTCTTTTCTCTATTAAATG 935

RESULT 8
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
; US-09-134-001C-1710

Query Match 100.0%; Score 21; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTAAATG 21
Db 976 TTTCTTTTCTCTATTAAATG 956

RESULT 9
US-09-297-648-4022/c
; Sequence 4022, Application US/09297648
; Patent No. 6964868
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassan, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
```

APPLICANT: Kita, David
 APPLICANT: Garcia, Veronica
 APPLICANT: Jones, William Lee
 APPLICANT: Stache-Crain, Biljit
 TITLE OF INVENTION: No. 69648681 Human Genes and Gene Expression
 TITLE OF INVENTION: Products II

FILE REFERENCE: 2300-1481
 CURRENT APPLICATION NUMBER: US/09/237,648
 CURRENT FILING DATE: 2000-03-10
 PRIOR APPLICATION NUMBER: 60/072,910
 PRIOR FILING DATE: 1998-01-28
 PRIOR APPLICATION NUMBER: 60/075,954
 PRIOR FILING DATE: 1998-02-24
 PRIOR APPLICATION NUMBER: 60/080,666
 PRIOR FILING DATE: 1998-04-03
 PRIOR APPLICATION NUMBER: 60/080,515
 PRIOR FILING DATE: 1998-04-03
 PRIOR APPLICATION NUMBER: 60/080,114
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/105,234
 PRIOR FILING DATE: 1998-10-21
 NUMBER OF SEQ ID NOS: 5252
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4022
 LENGTH: 781
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)...(781)
 OTHER INFORMATION: n = A,T,C or G

US-09-297-648-4022
 Query Match 92.4%; Score 19.4; DB 4; Length 781;
 Best Local Similarity 95.2%; Pred. No. 2.4e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
 ||||| ||||| ||||| ||||| |||||
 Db 474 TTTTCATTCTCTATTATG 454

RESULT 10
 US-08-956-171E-404/c
 Sequence 404, Application US/08956171E
 Patent No. 6593114

GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/956,171E
 FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/781,986
 FILING DATE: January 3, 1997
 ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (240) 314-1224
 TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 404:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6254 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 404:
 US-08-956-171E-404

Query Match 92.4%; Score 19.4; DB 3; Length 6254;
 Best Local Similarity 95.2%; Pred. No. 2.3e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
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 Db 2565 TTTTCTTTTCTCTATTATG 2545

RESULT 11
 US-08-781-986A-404/c
 Sequence 404, Application US/08781986A
 Patent No. 6737248

GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5255
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A
 FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PB248PP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 404:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6254 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

US-08-781-986A-404
 Query Match 92.4%; Score 19.4; DB 3; Length 6254;
 Best Local Similarity 95.2%; Pred. No. 2.3e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAG 21
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DB 2565 TTTTCTTTTCTCTATTAAAG 2545

RESULT 12
US-09-949-016-14387
; Sequence 14387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14387
; LENGTH: 23174
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14387

Query Match 92.4%; Score 19.4; DB 3; Length 23174;
Best Local Similarity 95.2%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAG 21
|||||
DB 6412 TTTTCTTTTCTCTATTAAAG 6432

RESULT 13
US-09-949-016-12235
; Sequence 12235, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12235
; LENGTH: 23187
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12235

Query Match 92.4%; Score 19.4; DB 3; Length 23187;
Best Local Similarity 95.2%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAG 21
|||||
DB 6427 TTTTCTTTTCTCTATTAAAG 6447

RESULT 14
US-09-328-352-1787/c
; Sequence 1787, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1787
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1787

Query Match 87.6%; Score 18.4; DB 3; Length 459;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
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DB 419 TTTTCTTTTCTCTATTAAAT 400

RESULT 15

US-09-949-016-182944/c
; Sequence 182944, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182944
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-182944

Query Match 87.6%; Score 18.4; DB 3; Length 589;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTTCTTTTCTCTATTAAATG 21
|||||
DB 549 TTTTCTTTTCTCTATTAAATG 530

Search completed: May 31, 2006, 21:13:02
Job time : 48.9259 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 545.568 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21

Sequence: 1 ttttttttttcttataatg 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	21	100.0	21	3	US-09-865-579A-10
2	21	100.0	21	3	Sequence 10, Appl
3	21	100.0	39	3	US-09-865-579A-20
4	21	100.0	1957	9	US-09-865-579A-27
5	21	100.0	2007	3	US-10-479-674-82
6	21	100.0	2007	3	US-09-452-599-169
7	21	100.0	2007	7	US-10-121-120-169
8	21	100.0	2007	9	US-10-479-674-78
9	21	100.0	2007	9	US-10-479-674-91
10	21	100.0	2007	9	US-10-121-120-169
11	21	100.0	2028	8	US-10-724-972A-3141
12	19.4	92.4	699	3	US-09-815-242-4505
13	19.4	92.4	699	3	US-09-815-242-4505
14	19.4	92.4	699	8	US-10-815-242-8471
15	19.4	92.4	781	10	US-10-282-122A-7879
16	19.4	92.4	6254	2	US-10-779-543-4866
17	19.4	92.4	6254	8	US-08-781-986A-404
18	19.4	92.4	6254	8	US-10-329-624-404

18	19	90.5	623	6	US-10-027-632-113610	Sequence 113610,
19	19	90.5	623	6	US-10-027-632-113611	Sequence 113611,
20	19	90.5	623	7	US-10-027-632-113610	Sequence 113610,
21	19	90.5	623	7	US-10-027-632-113611	Sequence 113611,
22	19	90.5	1203	4	US-09-925-065A-88445	Sequence 88445, A
23	19	90.5	1203	5	US-09-925-065A-88445	Sequence 88445, A
24	19	90.5	1203	12	US-10-301-480-189686	Sequence 189686,
25	19	90.5	1203	12	US-10-301-480-803095	Sequence 803095,
26	18.4	87.6	43	9	US-10-741-849-101	Sequence 101, App
27	18.4	87.6	170	8	US-10-424-599-22484	Sequence 22484, A
28	18.4	87.6	369	4	US-09-925-065A-261289	Sequence 261289,
29	18.4	87.6	369	5	US-09-925-065A-261289	Sequence 261289,
30	18.4	87.6	453	8	US-10-282-122A-8499	Sequence 8499, Ap
31	18.4	87.6	530	9	US-10-357-930-52735	Sequence 52735, A
32	18.4	87.6	623	4	US-09-925-065A-534873	Sequence 534873,
33	18.4	87.6	623	5	US-09-925-065A-534873	Sequence 534873,
34	18.4	87.6	762	4	US-09-925-065A-714264	Sequence 714264,
35	18.4	87.6	762	5	US-09-925-065A-714264	Sequence 714264,
36	18.4	87.6	978	7	US-10-369-493-40382	Sequence 40382, A
37	18.4	87.6	1999	10	US-10-481-032A-797	Sequence 797, App
38	18.4	87.6	2000	3	US-09-938-842A-4244	Sequence 4244, Ap
39	18.4	87.6	2000	3	US-09-938-842A-4244	Sequence 4244, Ap
40	18.4	87.6	2198	10	US-10-481-032A-698	Sequence 698, App
41	18.4	87.6	2395	10	US-10-750-185-26666	Sequence 26666, A
42	18.4	87.6	2395	10	US-10-750-623-26666	Sequence 26666, A
43	18.4	87.6	3650	10	US-10-793-626-3756	Sequence 3756, Ap
44	18.4	87.6	274869	9	US-10-741-600-17650	Sequence 17650, A
45	18.4	87.6	301692	7	US-10-428-487-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-865-579A-10
; Sequence 10, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; FILE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 958-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-10

Query Match 100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
|||||
Db 1 TTTTCTTTTCTCTATTATG 21

RESULT 2

US-09-865-579A-20
; Sequence 20, Application US/09865579A

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; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saico, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-20

Query Match          100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 1 TTTTCTTTTCTCTATTAAATG 21

RESULT 3
US-09-865-579A-27
; Sequence 27, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saico, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-27

Query Match          100.0%; Score 21; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 1 TTTTCTTTTCTCTATTAAATG 21

RESULT 4
US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
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; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIST
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match          100.0%; Score 21; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 905 TTTTCTTTTCTCTATTAAATG 885

RESULT 5
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match          100.0%; Score 21; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 6
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
```

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-10-121-120-169

Query Match 100.0%; Score 21; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 TTTTCTTTTCTCTATTATG 21
Db 955 TTTTCTTTTCTCTATTATG 935

RESULT 7

US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Inflectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-10-479-674-78

Query Match 100.0%; Score 21; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 TTTTCTTTTCTCTATTATG 21
Db 955 TTTTCTTTTCTCTATTATG 935

RESULT 8

US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Inflectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-10-479-674-90

Query Match 100.0%; Score 21; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 TTTTCTTTTCTCTATTATG 21
Db 955 TTTTCTTTTCTCTATTATG 935

RESULT 9

US-10-479-674-91/c
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Inflectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-10-479-674-91

Query Match 100.0%; Score 21; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 TTTTCTTTTCTCTATTATG 21
Db 955 TTTTCTTTTCTCTATTATG 935

RESULT 10

US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

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US-10-121-120-169
Query Match          100.0%; Score 21; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
    |||||||
Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 11
US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match          100.0%; Score 21; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
    |||||||
Db 976 TTTTCTTTTCTCTATTAAATG 956

RESULT 12
US-09-815-242-4505/c
; Sequence 4505, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8471
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(699)
US-09-815-242-8471

Query Match          92.4%; Score 19.4; DB 3; Length 699;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
    |||||||
Db 491 TTTTCTTTTCTCTATTCAATG 471

RESULT 13
US-09-815-242-8471/c
; Sequence 8471, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8471
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(699)
US-09-815-242-8471

Query Match          92.4%; Score 19.4; DB 3; Length 699;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
    |||||||
Db 491 TTTTCTTTTCTCTATTCAATG 471

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RESULT 14

US-10-282-122A-7879/c
; Sequence 7879, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/131,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7879
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-282-122A-7879

Query Match 92.4%; Score 19.4; DB 8; Length 699;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
|||||
DB 491 TTTTCTTTTCTCTATCAATG 471

RESULT 15

US-10-779-543-4866/c
; Sequence 4866, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALY EXPRESSED
; FILE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555

; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4866
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4, 5, 6, 7, 11, 13, 19, 584, 610, 690, 756
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-4866

Query Match 92.4%; Score 19.4; DB 10; Length 781;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
|||||
DB 474 TTTTCTTTTCTCTATTAAATG 454

Search completed: May 31, 2006, 23:02:17
Job time : 546.568 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 8.03704 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21

Sequence: 1 ttttcttttctctattaatg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 5886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubna/US09_NEW_PUB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubna/PCT_NEW_PUB.seq.*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/pubna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.4	87.6	1433	6	US-10-953-349-12899 Sequence 12899, A
C 2	17.8	84.8	3118	7	US-11-293-697-386 Sequence 386, App
C 3	16.8	80.0	449	6	US-10-488-619-1987 Sequence 1987, App
C 4	16.8	80.0	1039	6	US-10-953-349-22805 Sequence 22805, A
C 5	16.8	80.0	2628	7	US-11-264-784-50 Sequence 50, Appl
C 6	16.8	80.0	2628	7	US-11-264-737-83 Sequence 83, Appl
C 7	16.4	78.1	1540	6	US-10-953-349-26656 Sequence 26656, A
C 8	16.2	77.1	876	6	US-10-953-349-10770 Sequence 10770, A
C 9	16.2	77.1	1379	6	US-10-511-937-506 Sequence 506, App
C 10	16.2	77.1	1429	6	US-10-953-349-4335 Sequence 4335, App
C 11	16.2	77.1	1508	6	US-10-953-349-9239 Sequence 9239, App
C 12	16.2	77.1	1848	6	US-10-524-648-25 Sequence 25, Appl
C 13	16.2	77.1	1848	6	US-10-953-349-8854 Sequence 8854, App
C 14	16.2	77.1	2082	6	US-10-953-349-22034 Sequence 22034, A
C 15	16.2	77.1	2864	6	US-10-370-953-1139 Sequence 139, App
C 16	16.2	77.1	3059	7	US-11-246-999-19 Sequence 19, Appl
C 17	16.2	77.1	3069	7	US-11-312-958-49 Sequence 49, Appl
C 18	16.2	77.1	3516	7	US-11-217-528-1696 Sequence 1696, App
C 19	15.8	75.2	333	7	US-11-217-529-79539 Sequence 79539, A
C 20	15.8	75.2	602	7	US-11-301-554-1564 Sequence 1564, App
C 21	15.8	75.2	967	6	US-10-953-349-25612 Sequence 25612, A
C 22	15.8	75.2	2370	7	US-11-293-697-1032 Sequence 1032, App
C 23	15.8	75.2	3231	7	US-11-217-529-76288 Sequence 76288, A
C 24	15.8	75.2	4015	7	US-11-293-697-627 Sequence 627, App
C 25	15.8	75.2	4465	6	US-10-505-928-528 Sequence 528, App

C 26	15.8	75.2	4465	6	US-10-511-937-460 Sequence 460, App
C 27	15.8	75.2	4856	6	US-10-505-928-242 Sequence 242, App
C 28	15.8	75.2	7065	6	US-10-505-928-596 Sequence 596, App
C 29	15.4	73.3	366	7	US-11-217-529-80588 Sequence 80588, A
C 30	15.4	73.3	908	6	US-10-953-349-762 Sequence 762, App
C 31	15.4	73.3	1434	6	US-10-953-349-24368 Sequence 24368, A
C 32	15.4	73.3	1960	7	US-11-293-697-1665 Sequence 1665, App
C 33	15.4	73.3	2565	6	US-10-953-349-8347 Sequence 8347, App
C 34	15.4	73.3	2787	7	US-10-953-697-1524 Sequence 1524, App
C 35	15.4	73.3	2991	7	US-11-293-697-5421 Sequence 5421, App
C 36	15.4	73.3	37426	6	US-10-473-173-32 Sequence 32, Appl
C 37	15.4	73.3	42999	7	US-11-284-877-17 Sequence 17, Appl
C 38	15.2	72.4	156	7	US-11-217-529-80094 Sequence 80094, A
C 39	15.2	72.4	261	6	US-10-473-173-430 Sequence 430, App
C 40	15.2	72.4	342	7	US-11-217-529-191052 Sequence 191052, A
C 41	15.2	72.4	390	7	US-11-217-529-78848 Sequence 78848, A
C 42	15.2	72.4	406	7	US-11-301-554-1150 Sequence 1150, App
C 43	15.2	72.4	546	7	US-11-217-529-79406 Sequence 79406, A
C 44	15.2	72.4	651	6	US-10-953-349-28191 Sequence 28191, A
C 45	15.2	72.4	653	6	US-10-953-349-14981 Sequence 14981, A

ALIGNMENTS

RESULT 1

US-10-953-349-12899/c
; Sequence 12899, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12899
; LENGTH: 1433
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-12899

Query Match 87.6%; Score 18.4; DB 6; Length 1433;
Best Local Similarity 95.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	TTTTCTTTTCTCTATTAT 20
DB	23	TTTTCTTTTCTCTATTAT 4

RESULT 2

US-11-293-697-386
; Sequence 386, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 3118
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-386

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Query Match      84.8%; Score 17.8; DB 7; Length 3118;
Best Local Similarity 90.5%; Pred. No. 77;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 2998 TTTTCTGTGTGCTATTAAATG 3018

RESULT 3
US-10-488-619-1987
; Sequence 1987, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1987
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1987

Query Match      80.0%; Score 16.8; DB 6; Length 449;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTCTATTAAAT 20
Db 10 TTTTCTTTTCTCTCTTTTAAAT 29

RESULT 4
US-10-953-349-22805
; Sequence 22805, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22805
; LENGTH: 1039
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22805

Query Match      80.0%; Score 16.8; DB 6; Length 1039;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
Db 1002 TTTTATTTTGTCTATTAAAT 1021

RESULT 5
US-11-264-784-50/c
; Sequence 50, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John

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; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: Rattus norvegicus (GenBank Accession No. AB071986)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(893)
; OTHER INFORMATION: C16/18 elongase
US-11-264-784-50

Query Match      80.0%; Score 16.8; DB 7; Length 2628;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
Db 957 TTTTCTTTTGTCTATTATT 938

RESULT 6
US-11-264-737-83/c
; Sequence 83, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn Qun
; TITLE OF INVENTION: DCOSEAHXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: Rattus norvegicus (GenBank Accession No. AB071986)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(893)
; OTHER INFORMATION: C16/18 elongase
US-11-264-737-83

Query Match      80.0%; Score 16.8; DB 7; Length 2628;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
Db 957 TTTTCTTTTGTCTATTATT 938

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RESULT 7
US-10-953-349-26656/c
; Sequence 26656, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26656
; LENGTH: 1540
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-26656

Query Match      78.1%; Score 16.4; DB 6; Length 1540;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATTA 18
Db 1507 TTTTCTTTTCTCTATCA 1490

RESULT 8
US-10-953-349-10770/c
; Sequence 10770, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10770
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10770

Query Match      77.1%; Score 16.2; DB 6; Length 876;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
Db 860 TTTTCTTTTCTTGTTAATG 840

RESULT 9
US-10-511-937-506/c
; Sequence 506, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 506
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-506

Query Match      77.1%; Score 16.2; DB 6; Length 1379;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
Db 1347 TTTTCTTTTCTCTTTTAAGG 1327

RESULT 10
US-10-953-349-4335
; Sequence 4335, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4335
; LENGTH: 1429
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4335

Query Match      77.1%; Score 16.2; DB 6; Length 1429;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
Db 1392 TTTTCTTTTCTCAATTAATG 1412

RESULT 11
US-10-953-349-9239
; Sequence 9239, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9239
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9239

Query Match      77.1%; Score 16.2; DB 6; Length 1508;
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Best Local Similarity 85.7%; Pred. No. 2.7e+02; DB 6; Length 1848;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
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Db 1466 TTTTATTCTCTCAATTAAATG 1486
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RESULT 12
US-10-524-648-25/c
; Sequence 25, Application US/10524648
; Publication No. US20060107352A1
; GENERAL INFORMATION:
; APPLICANT: Schopfer, Christel
; APPLICANT: Sauer, Matt
; APPLICANT: Klebsattel, Martin
; APPLICANT: Flachmann, Ralf
; TITLE OF INVENTION: Transgenic expression cassettes for expressing nucleic acids in
; TITLE OF INVENTION: the flower of plants
; FILE REFERENCE: 13173-00002-US
; CURRENT APPLICATION NUMBER: US/10/524,648
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: PCT/EP 03/008394
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: DE 102 38 979.9
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 47 599.7
; PRIOR FILING DATE: 2002-02-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Adonis palaestina
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(1702)
; OTHER INFORMATION: coding for epsilon cyclase
US-10-524-648-25

Query Match 77.1%; Score 16.2; DB 6; Length 1848;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
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Db 1838 TTTTCTTTTCTCTATTAAATG 1818
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RESULT 13
US-10-953-349-8554
; Sequence 8554, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8554
; LENGTH: 1973
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8554

Query Match 77.1%; Score 16.2; DB 6; Length 1973;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21

Db 1869 TTTTATTTTCTCTACTAAAG 1889
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RESULT 14
US-10-953-349-22034
; Sequence 22034, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22034
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22034

Query Match 77.1%; Score 16.2; DB 6; Length 2082;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
||||| ||||| ||||| ||||| |||||
Db 2008 TTTTCTTTTCTCTATTAAATG 2028
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RESULT 15
US-10-370-959-139/c
; Sequence 139, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0170MNM
; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 2864
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (141)...(2675)
US-10-370-959-139

Query Match 77.1%; Score 16.2; DB 6; Length 2864;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
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Db 2860 TTTTCTTTTCTATAATG 2840

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Job time : 9.03704 secs

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 44.6914 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579a-21
Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	20	100.0	59	3	US-09-109-329-3
C 2	20	100.0	89	3	US-09-109-329-4
C 3	20	100.0	108	3	US-09-109-329-13
C 4	20	100.0	2007	2	US-08-743-637B-169
C 5	20	100.0	2007	3	US-08-526-840B-169
C 6	20	100.0	2028	3	US-09-134-001C-1710
C 7	17.4	87.0	1469	3	US-09-976-594-948
C 8	16.8	84.0	1089	3	US-09-134-000C-2599
C 9	16	80.0	199	3	US-09-533-559-3113
C 10	15.8	79.0	515	3	US-09-621-976-785
C 11	15.8	79.0	601	3	US-09-949-016-13973
C 12	15.8	79.0	601	3	US-09-949-016-183836
C 13	15.8	79.0	601	3	US-09-949-016-183837
C 14	15.8	79.0	601	3	US-09-949-016-186494
C 15	15.8	79.0	601	3	US-09-949-016-202891
C 16	15.8	79.0	913	3	US-09-270-767-9914
C 17	15.8	79.0	9259	3	US-09-949-016-17013
C 18	15.8	79.0	15393	3	US-09-453-702B-191
C 19	15.8	79.0	15393	3	US-10-114-170-191
C 20	15.8	79.0	56678	3	US-09-949-016-17453
C 21	15.8	79.0	60589	3	US-09-949-016-17070
C 22	15.8	79.0	93778	3	US-09-949-016-15096
C 23	15.8	79.0	121234	3	US-09-949-016-14142

C 24	15.8	79.0	140315	3	US-09-949-016-14141	Sequence 14141, A
C 25	15.8	79.0	147840	3	US-09-949-016-15236	Sequence 15236, A
C 26	15.4	77.0	601	3	US-09-949-016-89272	Sequence 89272, A
C 27	15.4	77.0	601	3	US-09-949-016-89273	Sequence 89273, A
C 28	15.4	77.0	792	3	US-09-134-001C-2275	Sequence 2275, Ap
C 29	15.4	77.0	885	3	US-09-134-000C-332	Sequence 332, App
C 30	15.4	77.0	2862	3	US-09-710-279-4341	Sequence 4341, Ap
C 31	15.4	77.0	4877	3	US-09-566-921-8	Sequence 8, Appli
C 32	15.4	77.0	54649	3	US-09-949-016-15867	Sequence 15867, A
C 33	15.4	77.0	69701	3	US-09-949-016-14187	Sequence 14187, A
C 34	15.4	77.0	73308	3	US-09-949-016-16326	Sequence 16326, A
C 35	15.4	77.0	74881	3	US-09-949-016-15545	Sequence 15545, A
C 36	15.4	77.0	74914	3	US-09-949-016-12286	Sequence 12286, A
C 37	15.4	77.0	88950	3	US-09-949-016-17150	Sequence 17150, A
C 38	15.4	77.0	94133	3	US-09-949-016-11901	Sequence 11901, A
C 39	15.4	77.0	94133	3	US-09-949-016-12713	Sequence 12713, A
C 40	15.4	77.0	94135	3	US-09-949-016-15934	Sequence 15934, A
C 41	15.4	77.0	94135	3	US-09-949-016-15935	Sequence 15935, A
C 42	15.4	77.0	94135	3	US-09-949-016-15936	Sequence 15936, A
C 43	15.4	77.0	94135	3	US-09-949-016-15937	Sequence 15937, A
C 44	15.4	77.0	137753	3	US-09-949-016-17404	Sequence 17404, A
C 45	15.4	77.0	237510	3	US-09-949-016-14273	Sequence 14273, A

ALIGNMENTS

RESULT 1
US-09-109-329-3/c
; Sequence 3, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species

US-09-109-329-3
Query Match 100.0%; Score 20; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTGAATATCTTTGCC 20
|||||
DB 54 GTTAGTGAATATCTTTGCC 35

RESULT 2
US-09-109-329-4
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-4

Query Match          100.0%; Score 20; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 18 GTTAGTTGAATATCTTTGCC 37

RESULT 3
US-09-109-329-13/c
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; TITLE OF INVENTION: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-13

Query Match          100.0%; Score 20; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 74 GTTAGTTGAATATCTTTGCC 55

RESULT 4
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
```

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; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match          100.0%; Score 20; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 5
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
```



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; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match      100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 6
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      100.0%; Score 20; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 1001 GTTAGTTGAATATCTTTGCC 982

RESULT 7
US-09-976-594-948
; Sequence 948, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 948
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; LENGTH: 1469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 040576.1
US-09-976-594-948

Query Match      87.0%; Score 17.4; DB 3; Length 1469;
Best Local Similarity 94.7%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 19
Db 363 GTTAGTTGAATATCTTTGCC 381

RESULT 8
US-09-134-000C-2599/c
; Sequence 2599, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2599
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2599

Query Match      84.0%; Score 16.8; DB 3; Length 1089;
Best Local Similarity 90.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 626 GTTAGTTGAATATCTTTGCC 607

RESULT 9
US-09-533-559-3113/c
; Sequence 3113, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3113
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1)...(199)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-3113

Query Match 80.0%; Score 16; DB 3; Length 199;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTG 18
DB 94 TTAGTTGAATATCTTTG 78

RESULT 10

US-09-621-976-785
; Sequence 785, Application US/09621976
; Patent No. 6639083
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSEI.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 785
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 351..515
US-09-621-976-785

Query Match 79.0%; Score 15.8; DB 3; Length 515;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTG 19
DB 126 GTCTGTGAATATCTTTG 144

RESULT 11

US-09-949-016-123973
; Sequence 123973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123973
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-123973

Query Match 79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTG 19
DB 506 GTTTGAGAAATATCTTTG 524

RESULT 12

US-09-949-016-183836
; Sequence 183836, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183836
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183836

Query Match 79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTG 20
DB 388 TAAGTTTAATATCTTTG 406

RESULT 13

US-09-949-016-183837
; Sequence 183837, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183837
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183837

Query Match 79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTG 20
DB 326 TAAGTTTAATATCTTTG 344

RESULT 14

US-09-949-016-186494/c
 ; Sequence 186494, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 186494
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-186494

Query Match 79.0%; Score 15.8; DB 3; Length 601;
 Best Local Similarity 89.5%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGC 19
 DB 243 GTTAGTTGAATATCTTTGC 225

RESULT 15

US-09-949-016-202891/c
 ; Sequence 202891, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 202891
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-202891

Query Match 79.0%; Score 15.8; DB 3; Length 601;
 Best Local Similarity 89.5%; Pred. No. 2.6e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGC 19
 DB 45 GTTAGTTGAATGTTTTC 27

Search completed: May 31, 2006, 21:13:07
 Job time : 46.6914 secs

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
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 (without alignments)
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 Title: US-09-865-579A-21
 Perfect score: 20
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 Scoring table: IDENTITY_NUC
 Gapop 10.0, Gapext 1.0
 Searched: 18892170 seqs, 6143817638 residues
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 Minimum DB seq length: 0
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 Post-processing: Minimum Match 0%
 Maximum Match 100%
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 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-865-579A-11
2	20	100.0	20	3	Sequence 11, Appl
3	20	100.0	39	3	Sequence 28, Appl
4	20	100.0	39	7	US-10-382-328-3
5	20	100.0	1957	9	US-10-479-674-82
6	20	100.0	2007	3	US-09-452-599-169
7	20	100.0	2007	7	US-10-121-120-169
8	20	100.0	2007	9	US-10-479-674-78
9	20	100.0	2007	9	US-10-479-674-90
10	20	100.0	2007	9	US-10-479-674-91
11	20	100.0	2007	9	US-10-121-120-169
12	20	100.0	2028	8	US-10-724-972A-3141
13	17.4	87.0	369	3	US-09-770-791-376
14	17.4	87.0	50807	11	US-10-330-773-781
15	16.8	84.0	350	3	US-09-770-791-701
16	16.8	84.0	403	4	US-09-925-065A-209245
17	16.8	84.0	403	5	US-09-925-065A-209245

C 18	16.8	84.0	419	12	US-10-301-480-296740,
C 19	16.8	84.0	419	12	Sequence 910149,
C 20	16.8	84.0	16484	3	US-09-070-927A-158
C 21	16.4	82.0	1095	8	Sequence 158, App
C 22	16.4	82.0	1374	3	US-10-282-122A-36279
C 23	16.4	82.0	1374	3	Sequence 36279, A
C 24	16.4	82.0	1374	3	US-09-938-842A-4922
C 25	16.4	82.0	2001	7	Sequence 4922, Ap
C 26	16.4	82.0	2052	13	US-10-108-260A-143
C 27	16.4	82.0	4437	13	Sequence 143, App
C 28	16.4	82.0	4437	13	Sequence 8918, Ap
C 29	16.4	82.0	4437	13	Sequence 8917, Ap
C 30	16.4	82.0	505	4	US-09-925-065A-831697
C 31	16.4	82.0	505	4	Sequence 831697,
C 32	16.4	82.0	513	4	US-09-925-065A-835390
C 33	16.4	82.0	513	4	Sequence 835390,
C 34	16.4	82.0	560	4	US-09-925-065A-129376
C 35	16.4	82.0	560	4	Sequence 129376,
C 36	16.4	82.0	580	12	US-10-301-480-443275
C 37	16.4	82.0	580	12	Sequence 443275,
C 38	16.4	82.0	582	4	US-10-301-480-1056684
C 39	16.4	82.0	582	4	Sequence 1056684,
C 40	16.4	82.0	582	4	Sequence 373388,
C 41	16.4	82.0	584	12	US-10-301-480-226005
C 42	16.4	82.0	584	12	Sequence 226005,
C 43	16.4	82.0	989	12	US-10-301-480-839414
C 44	16.4	82.0	989	12	Sequence 839414,
C 45	16.4	82.0	989	12	US-10-301-480-586303
C 46	16.4	82.0	989	12	Sequence 586303,
C 47	16.4	82.0	989	12	US-10-301-480-1199712
C 48	16.4	82.0	989	12	Sequence 1199712,
C 49	16.4	82.0	989	12	Sequence 583482,
C 50	16.4	82.0	989	12	Sequence 583482,
C 51	16.4	82.0	989	12	US-10-301-480-1196891
C 52	16.4	82.0	989	12	Sequence 1196891,
C 53	16.4	82.0	989	12	Sequence 102642,
C 54	16.4	82.0	989	12	Sequence 102642,
C 55	16.4	82.0	989	12	Sequence 619276,

ALIGNMENTS

RESULT 1

US-09-865-579A-11
 ; Sequence 11, Application US/09865579A
 ; Patent No. US20020098492A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Taya, Toshiki
 ; APPLICANT: Ishiguro, Takahiko
 ; APPLICANT: Saito, Juichi
 ; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
 ; FILE REFERENCE: 9558-003-27
 ; CURRENT FILING DATE: 2001-05-29
 ; PRIOR APPLICATION NUMBER: US/09/865,579A
 ; PRIOR FILING DATE: 2000-05-29
 ; PRIOR APPLICATION NUMBER: JP 2000-163149
 ; PRIOR FILING DATE: 2000-05-29
 ; PRIOR APPLICATION NUMBER: JP 2000-179394
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
 ; OTHER INFORMATION: or RNA derived from said gene
 US-09-865-579A-11

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTACTTGAATATCTTGTCC 20

Db 1 GTTACTTGAATATCTTGTCC 20

RESULT 2

US-09-865-579A-21
 ; Sequence 21, Application US/09865579A

us-09-865-579a-21.rnpbm

us-09-865-579a-21

Patent No. US20020098492A1

GENERAL INFORMATION:

APPLICANT: YASUKAWA, Kiyoshi

TITLE OF INVENTION: UNARY AVIAN MYELOBLASTOSIS VIRUS REVERS TRANSCRIPTASE AND ITS US

FILE REFERENCE: Q74425

CURRENT APPLICATION NUMBER: US/10/382,328

CURRENT FILING DATE: 2003-03-06

PRIOR APPLICATION NUMBER: JP 2002-071841

PRIOR FILING DATE: 2002-03-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.2

SEQ ID NO 3

LENGTH: 39

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Probe

US-10-382-328-3

Query Match 100.0%; Score 20; DB 7; Length 39;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTGCC 20

Db 1 GTTAGTTGAATATCTTTGCC 20

RESULT 5

US-10-479-674-82/c

Sequence 82, Application US/10479674

Publication No. US20050019893A1

GENERAL INFORMATION:

APPLICANT: Infectio Diagnostic (I.D.I.) Inc.

APPLICANT: Huletsky, Ann

APPLICANT: Rosebach, Valery

TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIST

FILE REFERENCE: TV/12287.92

CURRENT APPLICATION NUMBER: US/10/479,674

CURRENT FILING DATE: 2003-12-02

PRIOR APPLICATION NUMBER: CA 2,348,042

PRIOR FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 233

SOFTWARE: PatentIn version 3.1

SEQ ID NO 82

LENGTH: 1957

TYPE: DNA

ORGANISM: Staphylococcus aureus

US-10-479-674-82

Query Match 100.0%; Score 20; DB 9; Length 1957;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTGCC 20

Db 930 GTTAGTTGAATATCTTTGCC 911

RESULT 6

US-09-452-599-169/c

Sequence 169, Application US/09452599

Patent No. US20020055101A1

GENERAL INFORMATION:

APPLICANT: Bergeron, Michel G.

APPLICANT: Ouellette, Marc

APPLICANT: Roy, Paul H.

TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers

TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial

TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical

TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

FILE REFERENCE: 12287.31

CURRENT APPLICATION NUMBER: US/09/452,599

CURRENT FILING DATE: 1999-12-01

us-09-865-579a-21.rnpbm

us-09-865-579a-21

Patent No. US20020098492A1

GENERAL INFORMATION:

APPLICANT: Taya, Toshiki

APPLICANT: Ishiguro, Takahiko

APPLICANT: Saito, Juichi

TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of

TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus

FILE REFERENCE: 9558-003-27

CURRENT APPLICATION NUMBER: US/09/865,579A

CURRENT FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: JP 2000-163149

PRIOR FILING DATE: 2000-05-29

PRIOR APPLICATION NUMBER: JP 2000-179394

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer

US-09-865-579A-21

Query Match 100.0%; Score 20; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTGCC 20

Db 1 GTTAGTTGAATATCTTTGCC 20

RESULT 3

US-09-865-579A-28

Sequence 28, Application US/09865579A

Patent No. US20020098492A1

GENERAL INFORMATION:

APPLICANT: Taya, Toshiki

APPLICANT: Ishiguro, Takahiko

APPLICANT: Saito, Juichi

TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of

TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus

FILE REFERENCE: 9558-003-27

CURRENT APPLICATION NUMBER: US/09/865,579A

CURRENT FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: JP 2000-163149

PRIOR FILING DATE: 2000-05-29

PRIOR APPLICATION NUMBER: JP 2000-179394

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 28

LENGTH: 39

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Probe

US-09-865-579A-28

Query Match 100.0%; Score 20; DB 3; Length 39;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTGCC 20

Db 1 GTTAGTTGAATATCTTTGCC 20

RESULT 4

US-10-382-328-3

Sequence 3, Application US/10382328

Publication No. US20030219729A1

; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match 100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 7

US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match 100.0%; Score 20; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 8

US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match 100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 9

US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match 100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 10

US-10-479-674-91/c
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match 100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 11
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match 100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 12
US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match 100.0%; Score 20; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 1001 GTTAGTTGAATATCTTTGCC 982

RESULT 13
US-09-770-791-376/c
; Sequence 376, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-791-376

Query Match 87.0%; Score 17.4; DB 3; Length 369;
Best Local Similarity 94.7%; Pred. No. 5.6e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTGCC 20
|||||
Db 353 TGAGTTGAATATCTTTGCC 335

RESULT 14
US-10-330-773-781
; Sequence 781, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 781
; LENGTH: 50807
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(50807)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-781

Query Match 87.0%; Score 17.4; DB 11; Length 50807;
Best Local Similarity 94.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 19
||||| |||||||
DB 50715 GTTAGTTGGATATCTTTGC 50733

RESULT 15
US-09-770-791-701
; Sequence 701, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 701
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-701

Query Match 84.0%; Score 16.8; DB 3; Length 350;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
||| |||||||
DB 281 GTTGGTTGAAGATCTTTGCC 300

Search completed: May 31, 2006, 23:02:25
Job time : 520.589 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 7.65432 Seconds
(without alignments)
307.732 Million cell updates

Title: US-09-865-579A-21

Perfect score: 20

Sequence: 1 gttagtgaatatctttgcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs. 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB sea length: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Post-Processing: Minimum Match 0% Maximum Match 100%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

- | Database | Table | Field | Value |
|----------|---|---------------|-------|
| 1: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US09 | NEW_PUB_seq.* | |
| 2: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US06 | NEW_PUB_seq.* | |
| 3: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US07 | NEW_PUB_seq.* | |
| 4: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US08 | NEW_PUB_seq.* | |
| 5: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/PCT_NEW | PUB_seq.* | |
| 6: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US10 | NEW_PUB_seq.* | |
| 7: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US11 | NEW_PUB_seq.* | |
| 8: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US06 | NEW_PUB_seq.* | |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	16.4	82.0	1358	6	US-10-953-349-18434	Sequence 18434, A
C 2	16.4	82.0	2001	7	US-11-293-697-143	Sequence 143, App
C 3	15.8	79.0	729	7	US-11-217-529-5581	Sequence 5581, Ap
C 4	15.8	79.0	1542	6	US-10-953-349-27685	Sequence 27685, A
C 5	15.8	79.0	2676	7	US-11-217-529-5102	Sequence 5102, Ap
C 6	15.4	77.0	1827	7	US-11-217-529-78826	Sequence 78826, A
C 7	15.4	77.0	3012	7	US-11-217-529-78176	Sequence 78176, A
C 8	15	75.0	2778	7	US-11-217-529-5649	Sequence 5649, Ap
C 9	14.8	74.0	757	6	US-10-488-619-1353	Sequence 1353, Ap
C 10	14.8	74.0	1617	7	US-11-217-529-1954	Sequence 1954, Ap
C 11	14.8	74.0	1723	6	US-10-953-349-32641	Sequence 32641, A
C 12	14.8	74.0	3115	7	US-11-301-554-802	Sequence 802, App
C 13	14.8	74.0	4637	7	US-11-301-554-804	Sequence 804, App
C 14	14.8	74.0	4947	7	US-11-217-529-1490	Sequence 1490, Ap
C 15	14.4	72.0	1257	7	US-11-217-529-1867	Sequence 1867, Ap
C 16	14.4	72.0	3939	7	US-11-217-529-78219	Sequence 78219, A
C 17	14.4	72.0	4176	7	US-11-217-529-76349	Sequence 76349, A
C 18	14.2	71.0	25	7	US-11-217-529-143573	Sequence 143573, A
C 19	14.2	71.0	381	7	US-11-301-554-755	Sequence 755, App
C 20	14.2	71.0	381	7	US-11-217-529-173514	Sequence 173514, A
C 21	14.2	71.0	420	7	US-11-217-529-80348	Sequence 80348, A
C 22	14.2	71.0	666	6	US-10-953-349-18013	Sequence 18013, A
C 23	14.2	71.0	963	7	US-11-217-529-76581	Sequence 76581, A
C 24	14.2	71.0	1148	6	US-10-953-349-4321	Sequence 4321, Ap
C 25	14.2	71.0	1507	6	US-10-953-349-36240	Sequence 36240, A

ALIGNMENTS

RESULT 1

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US-10-953-349-18434
; Sequence 18434, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRE
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18434
; LENGTH: 1258
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-18434

```

Query Match	82.0%	Score 16.4;	DB 6;	Length 1258;
Best Local Similarity	94.4%	Pred. No. 9.8;		
Matches 17;	Conservative	0;	Mismatches	1;
Indels	0;	Gaps	0;	

Qy 1 GTTAGTTGAATATCTTTG 18
|||
Dp 1234 GTTAGTTGAATCTCTTTG 1251

RESULT 2

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US-11-293-697-143/c
; Sequence 143, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-143

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```

Query Match      82.0%; Score 16.4; DB 7; Length 2001;
Best Local Similarity 94.4%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTGC 19
Db 87 TTATTGGAATATCTTTGC 70

RESULT 3
US-11-217-529-5581/c
; Sequence 5581, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5581
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5581

Query Match      79.0%; Score 15.8; DB 7; Length 729;
Best Local Similarity 89.5%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTGC 20
Db 627 TTCGTTGAATATCTTTGCC 609

RESULT 4
US-10-953-349-27685/c
; Sequence 27685, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27685
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-27685

Query Match      79.0%; Score 15.8; DB 6; Length 1542;
Best Local Similarity 89.5%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGC 19
Db 1050 GTAAGTTGAAATATCTTTGC 1032

RESULT 5
US-11-217-529-5102/c

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; Sequence 5102, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5102
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5102

Query Match      79.0%; Score 15.8; DB 7; Length 2676;
Best Local Similarity 89.5%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGC 19
Db 1319 GTTAGTGGTAATCTTTGC 1301

RESULT 6
US-11-217-529-78826/c
; Sequence 78826, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78826
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78826

Query Match      77.0%; Score 15.4; DB 7; Length 1827;
Best Local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TAGTTGAATATCTTTGC 19
Db 1361 TAGTTGAAATATCTTTGC 1345

RESULT 7
US-11-217-529-78176/c
; Sequence 78176, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO

```

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; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78176
; LENGTH: 3012
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78176

Query Match          77.0%; Score 15.4; DB 7; Length 3012;
Best Local Similarity 94.1%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTAGTTGAATATCTTT 17
        ||||| ||||| ||||| |||||
Db      101 GTTAGTTGAATATCTTT 85

RESULT 8
US-11-217-529-5649/c
; Sequence 5649, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5649
; LENGTH: 2778
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5649

Query Match          75.0%; Score 15; DB 7; Length 2778;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TTAGTTGAATATCTT 16
        ||||| ||||| ||||| |||||
Db      1159 TTAGTTGAATATCTT 1145

RESULT 9
US-10-488-619-1353
; Sequence 1353, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1353
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1353

Query Match          74.0%; Score 14.8; DB 6; Length 757;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 TAGTTGAATATCTTTGCC 20
        ||||| ||||| ||||| |||||
Db      440 TTGTTGACTATCTTTGCC 457

RESULT 10
US-11-217-529-1954
; Sequence 1954, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1954
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1954

Query Match          74.0%; Score 14.8; DB 7; Length 1617;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 TAGTTGAATATCTTTGCC 20
        ||||| ||||| ||||| |||||
Db      133 TATTGAAATATCTTTGCC 150

RESULT 11
US-10-953-349-32641/c
; Sequence 32641, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32641
; LENGTH: 1723
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-32641

Query Match          74.0%; Score 14.8; DB 6; Length 1723;
Best Local Similarity 88.9%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy 2 TTAGTTGAATATCTTTC 19
    |||||
Db 991 TTAGTTGAATATCTTGC 974

RESULT 12
US-11-301-554-802
; Sequence 802, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 802
; LENGTH: 3115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-802

Query Match 74.0%; Score 14.8; DB 7; Length 3115;
Best Local Similarity 88.9%; Pred. No. 62;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTC 18
    |||||
Db 623 GTTAGTTGAATATCTTTC 640

RESULT 13
US-11-301-554-804
; Sequence 804, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
```

```
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 804
; LENGTH: 4637
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-804

Query Match 74.0%; Score 14.8; DB 7; Length 4637;
Best Local Similarity 88.9%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTC 18
    |||||
Db 2145 GTTAGTTGAATATCTTTC 2162

RESULT 14
US-11-217-529-1490
; Sequence 1490, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
```

```

; SEQ ID NO 1490
; LENGTH: 4947
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1490

Query Match      74.0%; Score 14.8; DB 7; Length 4947;
Best Local Similarity 88.9%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TTAGTTGAATATCTTTC 19
Db      1638 TCAGTTGAATATCTTTC 1655

RESULT 15
US-11-217-529-1867/c
; Sequence 1867, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1867
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1867

Query Match      72.0%; Score 14.4; DB 7; Length 1257;
Best Local Similarity 93.8%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTAGTTGAATATCTT 16
Db      986 GTTATTGAATATCTT 971

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Search completed: May 31, 2006, 21:22:05
Job time : 8.65432 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 62.5679 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-22
Perfect score: 28
Sequence: 1 aaagaaaaagatgcaaaagatttcaa 28

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PC/TUS COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	59	3	US-09-109-329-3
2	28	100.0	89	3	US-09-109-329-4
3	28	100.0	108	3	US-09-109-329-13
4	28	100.0	2007	2	US-08-743-637B-169
5	28	100.0	2007	3	US-08-526-840B-169
6	28	100.0	2028	3	US-09-134-001C-1710
7	21.6	77.1	47	3	US-09-109-329-6
8	20.8	74.3	348	3	US-09-248-796A-1105
9	20.2	72.1	2754	3	US-09-248-796A-5244
10	20	71.4	29	3	US-09-109-957-4
11	20	71.4	29	3	US-09-109-957-5
12	20	71.4	29	3	US-09-109-329-1
13	20	71.4	29	3	US-09-109-329-2
14	20	71.4	29	3	US-09-109-329-5
15	20	71.4	29	3	US-09-109-329-7
16	20	71.4	29	3	US-09-109-329-8
17	20	71.4	36	3	US-09-109-329-14
18	20	71.4	36	3	US-09-109-329-15
19	20	71.4	144	3	US-09-513-999C-17797
20	20	71.4	2003	3	US-10-664-775-3
21	20	71.4	2267	3	US-10-664-775-5
22	20	71.4	2279	3	US-10-664-775-4
23	20	71.4	2316	3	US-09-248-796A-6622

Sequence 1, Appli
Sequence 1, Appli
Sequence 730, App
Sequence 573, App
Sequence 720, App
Sequence 15378, A
Sequence 11750, A
Sequence 16934, A
Sequence 12762, A
Sequence 15775, A
Sequence 15494, A
Sequence 16001, A
Sequence 9823, Ap
Sequence 12455, A
Sequence 12815, A
Sequence 13043, A
Sequence 2, Appli
Sequence 3560, Ap
Sequence 31698, A
Sequence 87733, A
Sequence 150341,
Sequence 199396,
US-10-664-775-1
US-08-149-096A-1
US-09-221-017B-730
US-09-949-003-573
US-09-949-003-720
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US-09-949-016-11750
US-09-949-016-16934
US-09-949-016-12762
US-09-949-016-15775
US-09-949-016-15494
US-09-949-016-16001
US-09-248-796A-9823
US-09-248-796A-12455
US-09-248-796A-12815
US-09-248-796A-13043
US-07-808-455A-2
US-09-974-300-3560
US-09-949-016-31698
US-09-949-016-87733
US-09-949-016-150341
US-09-949-016-199396

ALIGNMENTS

RESULT 1
US-09-109-329-3
; Sequence 3, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-3

Query Match 100.0%; Score 28; DB 3; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.13;
Matches 24; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGCCAAAGATATTCAA 28
|||||:|||||:|||||:|||||:|||||:
Db 22 AAAGAAAAAGATGCCAAAGAUUCAA 49

RESULT 2
US-09-109-329-4/c
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-4

Query Match          100.0%; Score 28; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 50 AAAGAAAAAGATGCGCAAGATATTCAA 23

RESULT 3
US-09-109-329-13
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE OF INVENTION: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-13

Query Match          100.0%; Score 28; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 42 AAAGAAAAAGATGCGCAAGATATTCAA 69

RESULT 4
US-08-743-637B-169
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FOR CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA

; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
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; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5500
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match          100.0%; Score 28; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 5
US-08-526-840B-169
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
```

; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGGCAAGATATTCAA 28
Db 948 AAAGAAAAAGATGGCAAGATATTCAA 975

RESULT 6

US-09-134-001C-1710
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGGCAAGATATTCAA 28
Db 969 AAAGAAAAAGATGGCAAGATATTCAA 996

RESULT 7

US-09-109-329-6
; Sequence 6, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; TITLE OF INVENTION: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 47

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-6

Query Match 77.1%; Score 21.6; DB 3; Length 47;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGGCAAGATATTCAA 28
Db 10 AAAGAAAAAGATGGCAAGAAAAAAA 37

RESULT 8

US-09-248-796A-1105
; Sequence 1105, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1105
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1105

Query Match 74.3%; Score 20.8; DB 3; Length 348;
Best Local Similarity 91.7%; Pred. No. 80;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAAAAAGATGGCAAGATATTCAA 28
Db 142 AAAGAAAGATGGCAAGATATTGAA 165

RESULT 9

US-09-248-796A-5244
; Sequence 5244, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5244
; LENGTH: 2754
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5244

Query Match 72.1%; Score 20.2; DB 3; Length 2754;
Best Local Similarity 88.0%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGGCAAGATATT 25
|||||
Db 1548 AATGACAAAACATGGCAAGATATT 1572

RESULT 10
US-09-109-957-4
; Sequence 4, Application US/09109957
; Patent No. 6136533
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Modrusean, Zora D.
; APPLICANT: Pische, Isabelle A.
; APPLICANT: Duck, Peter D.
; APPLICANT: Cloney, Lynn P.
; APPLICANT: Wong, Alfred C.K.
; TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
; FILE REFERENCE: 480094.419
; CURRENT APPLICATION NUMBER: US/09/109,957
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Solid Phase Synthesis
US-09-109-957-4

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGGCAAG 20
|||||
Db 10 AAAGAAAAAAGATGGCAAG 29

RESULT 11
US-09-109-957-5/c
; Sequence 5, Application US/09109957
; Patent No. 6136533
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Modrusean, Zora D.
; APPLICANT: Pische, Isabelle A.
; APPLICANT: Duck, Peter D.
; APPLICANT: Cloney, Lynn P.
; APPLICANT: Wong, Alfred C.K.
; TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
; FILE REFERENCE: 480094.419
; CURRENT APPLICATION NUMBER: US/09/109,957
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: Solid Phase Synthesis
US-09-109-957-5

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGGCAAG 20
|||||

Db 20 AAAGAAAAAAGATGGCAAG 1

RESULT 12
US-09-109-329-1
; Sequence 1, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; TITLE OF INVENTION: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-1

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGGCAAG 20
|||||
Db 10 AAAGAAAAAAGATGGCAAG 29

RESULT 13
US-09-109-329-2/c
; Sequence 2, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; TITLE OF INVENTION: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-2

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGGCAAG 20
|||||
Db 20 AAAGAAAAAAGATGGCAAG 1

RESULT 14
US-09-109-329-5
; Sequence 5, Application US/09109329
; Patent No. 6503709

; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-5

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGAAAAAGATGGCAAG 20
DB 10 AAAGAAAAAGATGGCAAG 29

RESULT 15
US-09-109-329-7
; Sequence 7, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-7

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGAAAAAGATGGCAAG 20
DB 10 AAAGAAAAAGATGGCAAG 29

Search completed: May 31, 2006, 21:13:04
Job time : 63.5679 secs

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: May 31, 2006, 21:16:53 ; Search time 727.424 Seconds
 (without alignments)
 472.976 Million cell updates/sec

Title: US-09-865-579A-22

Perfect score: 28

Sequence: 1 aaagaaaaaagatgcaagatattcaa 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	3	US-09-865-579A-22
2	28	100.0	39	3	Sequence 22, Appl
3	28	100.0	39	7	Sequence 28, Appl
4	28	100.0	1957	9	Sequence 3, Appl
5	28	100.0	2007	3	Sequence 82, Appl
6	28	100.0	2007	3	Sequence 169, Appl
7	28	100.0	2007	7	Sequence 169, Appl
8	28	100.0	2007	9	Sequence 78, Appl
9	28	100.0	2007	9	Sequence 90, Appl
10	28	100.0	2007	9	Sequence 91, Appl
11	28	100.0	2028	8	Sequence 169, Appl
12	22.8	81.4	618	9	Sequence 3141, Ap
13	21.6	77.1	576	12	Sequence 389, Appl
14	21.6	77.1	576	12	Sequence 16890, A
15	21.6	77.1	576	12	Sequence 16891, A
16	21.6	77.1	576	12	Sequence 310371, A
17	21.6	77.1	576	12	Sequence 310372, A
18	21.6	77.1	576	12	Sequence 630299, A

c 18	21.6	77.1	576	12	US-10-301-480-630300	Sequence 630300,
c 19	21.6	77.1	576	12	US-10-301-480-923780	Sequence 923780,
c 20	21.6	77.1	576	12	US-10-301-480-923781	Sequence 923781,
21	21.6	77.1	586	4	US-09-925-065A-225842	Sequence 225842,
22	21.6	77.1	586	4	US-09-925-065A-225843	Sequence 225843,
23	21.6	77.1	586	5	US-09-925-065A-225842	Sequence 225842,
24	21.6	77.1	586	5	US-09-925-065A-225843	Sequence 225843,
c 25	21.6	77.1	641	6	US-10-027-632-83702	Sequence 83702, A
c 26	21.6	77.1	641	6	US-10-027-632-83703	Sequence 83703, A
c 27	21.6	77.1	641	6	US-10-027-632-83704	Sequence 83704, A
c 28	21.6	77.1	641	6	US-10-027-632-83705	Sequence 83705, A
c 29	21.6	77.1	641	6	US-10-027-632-83706	Sequence 83706, A
c 30	21.6	77.1	641	6	US-10-027-632-83707	Sequence 83707, A
c 31	21.6	77.1	641	7	US-10-027-632-83708	Sequence 83708, A
c 32	21.6	77.1	641	7	US-10-027-632-83709	Sequence 83709, A
c 33	21.6	77.1	641	7	US-10-027-632-83710	Sequence 83710, A
c 34	21.6	77.1	641	7	US-10-027-632-83711	Sequence 83711, A
c 35	21.6	77.1	641	7	US-10-027-632-83712	Sequence 83712, A
c 36	21.6	77.1	641	7	US-10-027-632-83713	Sequence 83713, A
c 37	21.6	77.1	665	6	US-10-027-632-34239	Sequence 34239, A
c 38	21.6	77.1	665	6	US-10-027-632-34240	Sequence 34240, A
c 39	21.6	77.1	665	6	US-10-027-632-34241	Sequence 34241, A
c 40	21.6	77.1	665	7	US-10-027-632-34239	Sequence 34239, A
c 41	21.6	77.1	665	7	US-10-027-632-34240	Sequence 34240, A
c 42	21.6	77.1	665	7	US-10-027-632-34241	Sequence 34241, A
c 43	21.6	77.1	1277	4	US-09-925-065A-686913	Sequence 686913,
c 44	21.6	77.1	1277	4	US-09-925-065A-716679	Sequence 716679,
c 45	21.6	77.1	1277	5	US-09-925-065A-686913	Sequence 686913,

ALIGNMENTS

RESULT 1

US-09-865-579A-22

; Sequence 22, Application US/09865579A

; Patent No. US20020098492A1

; GENERAL INFORMATION:

; APPLICANT: Taya, Toshiki

; APPLICANT: Ishiguro, Takahiko

; APPLICANT: Saio, Juichi

; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of

; FILE REFERENCE: 9558-003-27

; CURRENT FILING DATE: 2001-05-29

; PRIOR FILING DATE: 2000-05-29

; PRIOR APPLICATION NUMBER: JP 2000-163149

; PRIOR FILING DATE: 2000-05-29

; PRIOR APPLICATION NUMBER: JP 2000-179394

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 22

; LENGTH: 28

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-09-865-579A-22

Query Match 100.0%; Score 28; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAAGAAAAAAGATGCAAGATATTCAA 28

|||||

Db 1 AAAGAAAAAAGATGCAAGATATTCAA 28

|||||

RESULT 2

US-09-865-579A-28/c

; Sequence 28, Application US/09865579A

; Patent No. US20020098492A1

```
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-28

Query Match      100.0%; Score 28; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 33 AAAGAAAAAGATGCGCAAGATATTCAA 6

RESULT 3
US-10-382-328-3/c
; Sequence 3, Application US/10392328
; Publication No. US20030219729A1
; GENERAL INFORMATION:
; APPLICANT: YASUKAWA, Kiyoshi
; TITLE OF INVENTION: UNARY AVIAN MYELOBLASTOSIS VIRUS REVERS TRANSCRIPTASE AND ITS USE
; FILE REFERENCE: Q74425
; CURRENT APPLICATION NUMBER: US/10/382,328
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: JP 2002-071841
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-10-382-328-3

Query Match      100.0%; Score 28; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 33 AAAGAAAAAGATGCGCAAGATATTCAA 6

RESULT 4
US-10-479-674-82
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTA
; FILE REFERENCE: TV/12287.92
```

```
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 28; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 898 AAAGAAAAAGATGCGCAAGATATTCAA 925

RESULT 5
US-09-452-599-169
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 6
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
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; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 28; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
   |||||
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 7
US-10-479-674-78
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
   |||||
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 8
US-10-479-674-90
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90
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Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
   |||||
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975
```

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RESULT 9
US-10-479-674-91
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91
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Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
   |||||
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975
```

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RESULT 10
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Quellet, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169
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Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
 |||||
 Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 11
 US-10-724-972A-3141
 ; Sequence 3141, Application US/10724972A
 ; Publication No. US20040147734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Doucette-Stamm, Lynn
 ; APPLICANT: Bush, David
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: PATH03-16
 ; CURRENT APPLICATION NUMBER: US/10/724, 972A
 ; CURRENT FILING DATE: 2003-12-01
 ; PRIOR APPLICATION NUMBER: 09/450, 969
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/134, 001
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: 60/064, 964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: 60/055, 779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 7544
 ; SEQ ID NO 3141
 ; LENGTH: 2028
 ; TYPE: DNA
 ; ORGANISM: S.epidermidis
 US-10-724-972A-3141

Query Match 100.0%; Score 28; DB 8; Length 2028;
 Best Local Similarity 100.0%; Pred. No. 5.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
 |||||
 Db 969 AAAGAAAAAGATGCGCAAGATATTCAA 996

RESULT 12
 US-10-468-488-389/c
 ; Sequence 389, Application US/10468488
 ; Publication No. US20040234968A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CROTEAU, Rodney B.
 ; APPLICANT: LANGE, Bernd M.
 ; APPLICANT: WILDUNG, Mark R.
 ; TITLE OF INVENTION: PLANT OIL GLAND NUCLEIC ACID MOLECULES, AND METHODS OF
 ; FILE OF INVENTION: USE
 ; FILE REFERENCE: WSUR121565
 ; CURRENT APPLICATION NUMBER: US/10/468, 488
 ; CURRENT FILING DATE: 2003-08-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/02567
 ; PRIOR FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: 60/177, 264
 ; PRIOR FILING DATE: 2000-01-20
 ; NUMBER OF SEQ ID NOS: 473
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 389
 ; LENGTH: 618
 ; TYPE: DNA
 ; ORGANISM: Mentha piperita
 US-10-468-488-389

Query Match 81.4%; Score 22.8; DB 9; Length 618;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCC 26
 |||||
 Db 552 AAAGAAAAAGATGCGCAAGATATTCC 527

RESULT 13
 US-10-301-480-16890/c
 ; Sequence 16890, Application US/10301480
 ; Publication No. US20060057564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
 ; FILE OF INVENTION: in the Human Genome
 ; FILE REFERENCE: 108827.137
 ; CURRENT APPLICATION NUMBER: US/10/301,480
 ; CURRENT FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 10/215,598
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: US 60/311,695
 ; PRIOR FILING DATE: 2001-08-10
 ; NUMBER OF SEQ ID NOS: 1226818
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16890
 ; LENGTH: 576
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-301-480-16890

Query Match 77.1%; Score 21.6; DB 12; Length 576;
 Best Local Similarity 85.7%; Pred. No. 8.6e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
 |||||
 Db 130 AAAGAAAAAGATGTAAGAAAGCTATTCAA 103

RESULT 14
 US-10-301-480-16891/c
 ; Sequence 16891, Application US/10301480
 ; Publication No. US20060057564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
 ; FILE OF INVENTION: in the Human Genome
 ; FILE REFERENCE: 108827.137
 ; CURRENT APPLICATION NUMBER: US/10/301,480
 ; CURRENT FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 10/215,598
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: US 60/311,695
 ; PRIOR FILING DATE: 2001-08-10
 ; NUMBER OF SEQ ID NOS: 1226818
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16891
 ; LENGTH: 576
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-301-480-16891

Query Match 77.1%; Score 21.6; DB 12; Length 576;
 Best Local Similarity 85.7%; Pred. No. 8.6e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
 |||||
 Db 130 AAAGAAAAAGATGTAAGAAAGCTATTCAA 103

RESULT 15
 US-10-301-480-310371/c
 ; Sequence 310371, Application US/10301480
 ; Publication No. US20060057564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 310371
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-310371

Query Match 77.1%; Score 21.6; DB 12; Length 576;
Best Local Similarity 85.7%; Pred. No. 8.6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
||| ||||| ||||| ||||| ||||| |||||
Db 130 AAAAAAAAGATGTAAGCTATTCAA 103

Search completed: May 31, 2006, 23:02:18
Job time : 728.424 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 10.716 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-22
Perfect score: 28
Sequence: 1 aaagaaaaagatgcaagatttcaa 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB_seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB_seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB_seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB_seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB_seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB_seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB_seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	67.9	522	7	US-11-217-529-75813
2	19	67.9	644	6	US-10-953-349-29445
3	19	67.9	987	7	US-11-217-529-191045
4	19	67.9	1289	6	US-10-953-349-23125
5	19	67.9	1448	6	US-10-953-349-17539
6	19	67.9	1578	7	US-11-217-529-78085
7	18.6	66.4	549	7	US-11-217-529-79689
8	18.6	66.4	1116	7	US-11-217-529-2228
9	18.6	66.4	2568	7	US-11-217-529-77262
10	18.4	65.7	1574	6	US-10-953-349-8516
11	18.4	65.7	1664	6	US-10-953-349-8747
12	18.4	65.7	1777	6	US-10-953-349-9966
13	18.4	65.7	1801	6	US-10-953-349-935
14	18.4	65.7	2490	7	US-11-293-697-401
15	18.4	65.7	3949	7	US-11-293-697-1211
16	18.4	65.7	4422	7	US-11-217-529-3003
17	18.4	65.7	4422	7	US-11-217-529-3003
18	18.2	65.0	682	6	US-10-488-619-2641
19	18.2	65.0	2667	7	US-11-217-529-81093
20	18	64.3	1176	7	US-11-217-529-80878
21	18	64.3	1187	6	US-10-953-349-1243
22	17.8	63.6	387	7	US-11-217-529-5325
23	17.8	63.6	1281	7	US-11-217-529-3303
24	17.8	63.6	2140	7	US-11-293-697-1100
25	17.6	62.9	558	6	US-10-953-349-28180

26	17.6	62.9	1407	7	US-11-217-529-535	Sequence 535, App
27	17.6	62.9	1476	6	US-10-953-349-33236	Sequence 33236, A
28	17.6	62.9	2019	7	US-11-217-529-79218	Sequence 79218, A
29	17.6	62.9	2021	6	US-10-953-349-14571	Sequence 14571, A
30	17.4	62.1	600	7	US-11-217-529-466	Sequence 466, App
31	17.4	62.1	750	7	US-11-217-529-81373	Sequence 81373, A
32	17.4	62.1	791	6	US-10-953-349-21923	Sequence 21923, A
33	17.4	62.1	1127	6	US-10-953-349-1769	Sequence 1769, App
34	17.4	62.1	1250	6	US-10-473-173-69	Sequence 69, Appl
35	17.4	62.1	1661	6	US-10-953-349-1884	Sequence 1884, App
36	17.4	62.1	1700	6	US-10-953-349-2065	Sequence 2065, App
37	17.4	62.1	1716	7	US-11-217-529-77529	Sequence 77529, A
38	17.4	62.1	1854	7	US-11-217-529-78308	Sequence 78308, A
39	17.4	62.1	2897	7	US-11-217-529-883	Sequence 883, App
40	17.4	62.1	2853	6	US-10-953-349-6444	Sequence 6444, App
41	17.4	62.1	4098	6	US-10-510-508-2	Sequence 2, Appl1
42	17.4	62.1	4260	7	US-11-217-529-2191	Sequence 2191, App
43	17.4	62.1	6891	7	US-11-251-724-2	Sequence 2, Appl1
44	17.2	61.4	25	7	US-11-217-529-11035	Sequence 11035, A
45	17.2	61.4	25	7	US-11-217-529-163683	Sequence 163683,

ALIGNMENTS

RESULT 1
US-11-217-529-75813
; Sequence 75813, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75813
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75813
Query Match 67.9%; Score 19; DB 7; Length 522;
Best Local Similarity 81.5%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 AAGAAAAAGATGGCAAGATATTCAA 28
DB 442 AAGAAAAAGATGGCAAGATATTCAA 468
RESULT 2
US-10-953-349-29445/c
; Sequence 29445, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29445


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; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79689
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79689

Query Match          66.4%; Score 18.6; DB 7; Length 549;
Best Local Similarity 84.0%; Pred. No. 50;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGGCAAGATATT 25
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Db 412 AAAGAACACTAAGGCAAGATATT 436

RESULT 8
US-11-217-529-2228
; Sequence 2228, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2228
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2228

Query Match          66.4%; Score 18.6; DB 7; Length 1116;
Best Local Similarity 84.0%; Pred. No. 56;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGGCAAGATATT 25
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Db 147 AAAGAAATACGAAGGCCAAGATATT 171

RESULT 9
US-11-217-529-77262
; Sequence 77262, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285

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DB      1499 AGAAACAAAGATGAAAGAGATTCAA 1472
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RESULT 12
US-10-953-349-8747/c
; Sequence 8747, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8747
; LENGTH: 1664
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8747

Query Match      65.7%; Score 18.4; DB 6; Length 1664;
Best Local Similarity 78.6%; Pred. No. 71;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AAAGAAAAAGATGCGCAAGATATTCAA 28
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DB      1571 AAAGAAACAGATATATAACATATGCAA 1544
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RESULT 13
US-10-953-349-9966/c
; Sequence 9966, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9966
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9966

Query Match      65.7%; Score 18.4; DB 6; Length 1777;
Best Local Similarity 78.6%; Pred. No. 72;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
DB      403 AGAGAAAGAGACGACCAAGATAGTCAA 376
|||||

RESULT 14
US-10-953-349-935/c
; Sequence 935, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 935
; LENGTH: 1801
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-935

Query Match      65.7%; Score 18.4; DB 6; Length 1801;
Best Local Similarity 78.6%; Pred. No. 72;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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; SEQ ID NO 935
; LENGTH: 1801
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-935

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Best Local Similarity 78.6%; Pred. No. 72;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
DB      430 AGAGAAAGAGACGACCAAGATAGTCAA 403
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RESULT 15
US-11-293-697-401
; Sequence 401, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 401
; LENGTH: 2490
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-401

Query Match      65.7%; Score 18.4; DB 7; Length 2490;
Best Local Similarity 78.6%; Pred. No. 76;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AAAGAAAAAGATGCGCAAGATATTCAA 28
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DB      695 AAACAATTAATTGTCAAGAAATTCAA 722
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Search completed: May 31, 2006, 21:22:04
Job time : 10.716 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 44.6914 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-23

Perfect score: 20

Sequence: 1 ttctttttatcttcggta 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTRUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	20	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	20	100.0	2028	3	US-09-134-001C-1710 Sequence 1710, Ap
C 4	17.4	87.0	601	3	US-09-949-016-82367 Sequence 82367, A
C 5	17.4	87.0	601	3	US-09-949-016-82368 Sequence 82368, A
C 6	17.4	87.0	601	3	US-09-949-016-82369 Sequence 82369, A
C 7	17.4	87.0	601	3	US-09-949-016-82370 Sequence 82370, A
C 8	17.4	87.0	601	3	US-09-949-016-187537 Sequence 187537, A
C 9	17.4	87.0	601	3	US-09-949-016-187538 Sequence 187538, A
C 10	17.4	87.0	601	3	US-09-949-016-187539 Sequence 187539, A
C 11	17.4	87.0	601	3	US-09-949-016-187540 Sequence 187540, A
C 12	17.4	87.0	910	5	US-09-974-300-1089 Sequence 1089, Ap
C 13	17.4	87.0	98962	3	US-09-949-016-14133 Sequence 14133, A
C 14	17.4	87.0	102884	3	US-09-949-016-17100 Sequence 17100, A
C 15	16.8	84.0	601	3	US-09-949-016-153600 Sequence 153600, A
C 16	16.8	84.0	795	3	US-09-248-796A-3644 Sequence 3644, Ap
C 17	16.8	84.0	823	3	US-09-949-016-2333 Sequence 2333, Ap
C 18	16.8	84.0	1214	3	US-09-506-286B-15 Sequence 15, Appl
C 19	16.8	84.0	1214	3	US-09-506-286B-18 Sequence 18, Appl
C 20	16.8	84.0	1214	3	US-09-762-861B-15 Sequence 15, Appl
C 21	16.8	84.0	1214	3	US-09-762-861B-18 Sequence 18, Appl
C 22	16.8	84.0	1214	3	US-10-065-133A-15 Sequence 15, Appl
C 23	16.8	84.0	1214	3	US-10-065-133A-18 Sequence 18, Appl

C 24 16.8 84.0 1214 3 US-10-434-811A-15 Sequence 15, Appl
C 25 16.8 84.0 1214 3 US-10-434-811A-18 Sequence 18, Appl
C 26 16.8 84.0 1214 3 US-09-506-286B-13 Sequence 13, Appl
C 27 16.8 84.0 1241 3 US-09-506-286B-16 Sequence 16, Appl
C 28 16.8 84.0 1241 3 US-09-762-861B-13 Sequence 13, Appl
C 29 16.8 84.0 1241 3 US-09-762-861B-16 Sequence 16, Appl
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C 31 16.8 84.0 1241 3 US-10-065-133A-16 Sequence 16, Appl
C 32 16.8 84.0 1241 3 US-10-434-811A-13 Sequence 13, Appl
C 33 16.8 84.0 1241 3 US-10-434-811A-16 Sequence 16, Appl
C 34 16.8 84.0 2277 3 US-09-506-286B-46 Sequence 46, Appl
C 35 16.8 84.0 2277 3 US-09-506-286B-49 Sequence 49, Appl
C 36 16.8 84.0 2277 3 US-10-065-133A-46 Sequence 46, Appl
C 37 16.8 84.0 2277 3 US-10-065-133A-49 Sequence 49, Appl
C 38 16.8 84.0 2341 3 US-09-506-286B-44 Sequence 44, Appl
C 39 16.8 84.0 2341 3 US-09-506-286B-47 Sequence 47, Appl
C 40 16.8 84.0 2341 3 US-10-065-133A-44 Sequence 44, Appl
C 41 16.8 84.0 2341 3 US-10-065-133A-47 Sequence 47, Appl
C 42 16.8 84.0 3116 3 US-09-710-279-3721 Sequence 3721, Ap
C 43 16.8 84.0 3598 3 US-09-710-279-4216 Sequence 4216, Ap
C 44 16.8 84.0 12951 3 US-09-949-016-14075 Sequence 14075, A
C 45 16.8 84.0 15071 3 US-09-710-279-2963 Sequence 2963, Ap

ALIGNMENTS

RESULT 1

US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 2007;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 1167 TTCTTTTATCTTCGGTTA 1148

RESULT 2
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSER: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 2007;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 1167 TTCTTTTATCTTCGGTTA 1148

RESULT 3
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370

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; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 2028;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 1188 TTCTTTTATCTTCGGTTA 1169

RESULT 4
US-09-949-016-82367
; Sequence 82367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82367
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82367

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 3; Length 601;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
Db 129 TTCTTTTATCTTCGTGT 147

RESULT 5
US-09-949-016-82368
; Sequence 82368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82368
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82368

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Query Match	87.0%	Score 17.4;	DB 3;	Length 601;
Best Local Similarity	94.7%	Pred. No. 4e+02;		
Matches 18;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

Qy 1 T T C T T T T T T A T C T T C G G T T 19
db 130 T T C T T T T T T A T C T T C T G T T 148

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RESULT 6
US-09-949-016-82369
; Sequence 82369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 82369
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82369

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Query Match	87.0%	Score 17.4;	DB 3;	Length 601;
Best Local Similarity	94.7%	Pred. No. 4e+02;		
Matches 18;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 1 TTCTTTTATCTTCGGTT 19
Db 255 TTCTTTTATCTTCGTT 273

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RESULT 7
US-09-949-016-82370
; Sequence 82370, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 82370
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82370

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Query Match	87.0%	Score 17.4;	DB 3;	Length 601;
Best Local Similarity	94.7%;	Pred. No. 4e+02;		
Matches 18;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 1 TTCTTTTATCTTCGGTT 19
Db 479 TTCTTTTATCTTCGGTT 497

RESULT 8
US-09-949-016-187537
; Sequence 187537, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 187537
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187537

Query Match	87.0%	Score 17.4;	DB 3;	Length 601;
Best Local Similarity	94.7%;	Pred. No. 4e+02;		
Matches 18;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 1 TTCCTTTTATCTTCGGTT 19
|||
Db 129 TTCCTTTTATCTTCGTT 147

RESULT 9
US-09-949-016-187538
; Sequence 187538, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187538
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187538

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 3; Length 601;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
Db 130 TTCTTTTATCTTCGT 148

RESULT 10
US-09-949-016-187539
; Sequence 187539, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187539
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187539

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 3; Length 601;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
Db 255 TTCTTTTATCTTCGT 273

RESULT 11
US-09-949-016-187540
; Sequence 187540, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187540
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human

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US-09-949-016-187540

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 3; Length 601;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
Db 479 TTCTTTTATCTTCGT 497

RESULT 12
US-09-974-300-1089/c
; Sequence 1089, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE OF INVENTION: Expression
; FILE REFERENCE: 10085-500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1089
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1089

Query Match
Best Local Similarity 87.0%; Score 17.4; DB 5; Length 910;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
Db 552 TCCTTTTATCTTCGGTT 534

RESULT 13
US-09-949-016-14133/c
; Sequence 14133, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14133
; LENGTH: 9862
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(9862)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14133

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Query Match      87.0%; Score 17.4; DB 3; Length 98962;
Best Local Similarity 94.7%; Pred.No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  TTCTTTTATCTTCGGTT 19
      |||||
DB      47622 TTCTTTTATCTTCGTT 47604

RESULT 14
US-09-949-016-17100/c
; Sequence 17100, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,769
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17100
; LENGTH: 102884
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(102884)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17100

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GenCore version 5.1.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 519.589 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-23
Perfect score: 20
Sequence: 1 tctcttttatcttcggtta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18992170 seqs, 6143817638 residues

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Maximum Match 100%
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Database : Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	3	US-09-865-579A-13	Sequence 13, Appl
2	20	100.0	20	3	US-09-865-579A-23	Sequence 23, Appl
3	20	100.0	20	7	US-10-382-328-2	Sequence 2, Appl
4	20	100.0	85	10	US-10-995-051-19	Sequence 19, Appl
5	20	100.0	86	10	US-10-995-051-30	Sequence 30, Appl
C 6	20	100.0	281	10	US-10-995-051-14	Sequence 14, Appl
C 7	20	100.0	560	10	US-10-478-633A-151	Sequence 151, Appl
C 8	20	100.0	652	9	US-10-479-674-30	Sequence 30, Appl
C 9	20	100.0	657	9	US-10-479-674-27	Sequence 27, Appl
C 10	20	100.0	744	9	US-10-479-674-29	Sequence 29, Appl
C 11	20	100.0	782	9	US-10-479-674-28	Sequence 28, Appl
C 12	20	100.0	1858	9	US-10-479-674-191	Sequence 191, Appl
C 13	20	100.0	1861	9	US-10-479-674-192	Sequence 192, Appl
C 14	20	100.0	1861	9	US-10-479-674-193	Sequence 193, Appl
C 15	20	100.0	1957	9	US-10-479-674-82	Sequence 82, Appl
C 16	20	100.0	2007	3	US-09-452-593-169	Sequence 169, Appl
C 17	20	100.0	2007	7	US-10-121-120-169	Sequence 169, Appl

C 18	20	100.0	2007	9	US-10-479-674-78	Sequence 78, Appl
C 19	20	100.0	2007	9	US-10-479-674-90	Sequence 90, Appl
C 20	20	100.0	2007	9	US-10-479-674-91	Sequence 91, Appl
C 21	20	100.0	2007	9	US-10-121-120-169	Sequence 169, Appl
C 22	20	100.0	2028	8	US-10-724-972A-3141	Sequence 3141, App
C 23	20	100.0	2386	9	US-10-479-674-224	Sequence 224, App
C 24	20	100.0	2410	9	US-10-479-674-190	Sequence 190, App
C 25	20	100.0	2436	9	US-10-479-674-31	Sequence 31, Appl
C 26	20	100.0	3101	9	US-10-479-674-195	Sequence 195, App
C 27	20	100.0	3506	9	US-10-479-674-196	Sequence 196, App
C 28	18.4	92.0	86	10	US-10-995-051-13	Sequence 13, Appl
C 29	17.4	87.0	277	10	US-10-499-352A-301	Sequence 301, App
C 30	17.4	87.0	439	6	US-10-027-632-73528	Sequence 73528, A
C 31	17.4	87.0	439	6	US-10-027-632-75071	Sequence 75071, A
C 32	17.4	87.0	439	6	US-10-027-632-108842	Sequence 108842, A
C 33	17.4	87.0	439	7	US-10-027-632-73528	Sequence 73528, A
C 34	17.4	87.0	439	7	US-10-027-632-75071	Sequence 75071, A
C 35	17.4	87.0	439	7	US-10-027-632-108842	Sequence 108842, A
C 36	17.4	87.0	546	4	US-09-925-065A-475594	Sequence 475594, A
C 37	17.4	87.0	546	5	US-09-925-065A-475594	Sequence 475594, A
C 38	17.4	87.0	570	10	US-10-501-282-613	Sequence 613, App
C 39	17.4	87.0	582	10	US-10-499-352A-303	Sequence 303, App
C 40	17.4	87.0	614	12	US-10-301-480-197304	Sequence 197304, A
C 41	17.4	87.0	614	12	US-10-301-480-810713	Sequence 810713, A
C 42	17.4	87.0	633	10	US-10-499-352A-302	Sequence 302, App
C 43	17.4	87.0	639	4	US-09-925-065A-96207	Sequence 96207, A
C 44	17.4	87.0	639	5	US-09-925-065A-96207	Sequence 96207, A
C 45	17.4	87.0	910	3	US-09-974-300-1089	Sequence 1089, App

ALIGNMENTS

RESULT 1

US-09-865-579A-13
; Sequence 13, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiko
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saigo, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-13

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTCTTTTATCTTCGGTTA 20

DB 1 TCTCTTTTATCTTCGGTTA 20

RESULT 2

US-09-865-579A-23
; Sequence 23, Application US/09865579A

```
/ Patent No. US20020098492A1
/ GENERAL INFORMATION:
/ APPLICANT: Taya, Toshiki
/ APPLICANT: Ishiguro, Takahiko
/ APPLICANT: Saito, Juichi
/ TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
/ TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
/ FILE REFERENCE: 9558-003-27
/ CURRENT APPLICATION NUMBER: US/09/865,579A
/ CURRENT FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: JP 2000-163149
/ PRIOR FILING DATE: 2000-05-29
/ PRIOR APPLICATION NUMBER: JP 2000-179394
/ PRIOR FILING DATE: 2000-06-09
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 23
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
US-09-865-579A-23

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 1 TTCTTTTATCTTCGGTTA 20

RESULT 3
US-10-382-328-2
/ Sequence 2, Application US/10382328
/ Publication No. US20030219729A1
/ GENERAL INFORMATION:
/ APPLICANT: YASUKAWA, Kiyohshi
/ TITLE OF INVENTION: UNARY AVIAN MYELOBLASTOSIS VIRUS REVERS TRANSCRIPTASE AND ITS USE
/ FILE REFERENCE: Q74425
/ CURRENT APPLICATION NUMBER: US/10/382,328
/ PRIOR FILING DATE: 2003-03-06
/ PRIOR APPLICATION NUMBER: JP 2002-071841
/ PRIOR FILING DATE: 2002-03-15
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
US-10-382-328-2

Query Match          100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 1 TTCTTTTATCTTCGGTTA 20

RESULT 4
US-10-995-051-19
/ Sequence 19, Application US/10995051
/ Publication No. US20050250094A1
/ GENERAL INFORMATION:
/ APPLICANT: Storhoff, James
/ APPLICANT: Lucas, Adam
/ APPLICANT: Muller, Uwe
/ APPLICANT: Bao, Yijia P
```

```
/ TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination
/ TITLE OF INVENTION: and Scatter-Based Detection of Nanoparticle Probe Complexes
/ FILE REFERENCE: MBHB-03-466-E
/ CURRENT APPLICATION NUMBER: US/10/995,051
/ CURRENT FILING DATE: 2004-11-22
/ PRIOR APPLICATION NUMBER: 10/854,848
/ PRIOR FILING DATE: 2004-05-27
/ PRIOR APPLICATION NUMBER: 60/474,569
/ PRIOR FILING DATE: 2003-05-30
/ PRIOR APPLICATION NUMBER: 60/499,034
/ PRIOR FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: 60/517,450
/ PRIOR FILING DATE: 2003-11-04
/ PRIOR APPLICATION NUMBER: 60/567,874
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 19
/ LENGTH: 85
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: DNA target.
US-10-995-051-19
```

```
Query Match          100.0%; Score 20; DB 10; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 36 TTCTTTTATCTTCGGTTA 55
```

```
RESULT 5
US-10-995-051-30
/ Sequence 30, Application US/10995051
/ Publication No. US20050250094A1
/ GENERAL INFORMATION:
/ APPLICANT: Storhoff, James
/ APPLICANT: Lucas, Adam
/ APPLICANT: Muller, Uwe
/ APPLICANT: Bao, Yijia P
/ TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination
/ TITLE OF INVENTION: and Scatter-Based Detection of Nanoparticle Probe Complexes
/ FILE REFERENCE: MBHB-03-466-E
/ CURRENT APPLICATION NUMBER: US/10/995,051
/ CURRENT FILING DATE: 2004-11-22
/ PRIOR APPLICATION NUMBER: 10/854,848
/ PRIOR FILING DATE: 2004-05-27
/ PRIOR APPLICATION NUMBER: 60/474,569
/ PRIOR FILING DATE: 2003-05-30
/ PRIOR APPLICATION NUMBER: 60/499,034
/ PRIOR FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: 60/517,450
/ PRIOR FILING DATE: 2003-11-04
/ PRIOR APPLICATION NUMBER: 60/567,874
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 30
/ LENGTH: 86
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: DNA target
US-10-995-051-30

Query Match          100.0%; Score 20; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TTCTTTTATCTTCGGTTA 20
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Db 37 TTCTTTTATCTTCGGTTA 56
|||||

RESULT 6
US-10-995-051-14/c
; Sequence 14, Application US/10995051
; Publication No. US20050250094A1
; GENERAL INFORMATION:
; APPLICANT: Storhoff, James
; APPLICANT: Lucas, Adam
; APPLICANT: Muller, Uwe
; APPLICANT: Bao, Yijia P
; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination
; TITLE OF INVENTION: and Scatter-Based Detection of Nanoparticle Probe Complexes
; FILE REFERENCE: MEHB-03-466-E
; CURRENT APPLICATION NUMBER: US/10/995, 051
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 10/854, 848
; PRIOR FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: 60/474, 569
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 60/499, 034
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/517, 450
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: 60/567, 874
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Target Meca 4 is a meca 281 base-pair PCR amplicon.
US-10-995-051-14

Query Match 100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
|||||

Db 120 TTCTTTTATCTTCGGTTA 101
|||||

RESULT 7
US-10-478-633A-151/c
; Sequence 151, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; TITLE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478, 633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 151
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-151

Query Match 100.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
|||||

Db 147 TTCTTTTATCTTCGGTTA 128
|||||

RESULT 8
US-10-479-674-30/c
; Sequence 30, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479, 674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348, 042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-30

Query Match 100.0%; Score 20; DB 9; Length 652;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
|||||

Db 81 TTCTTTTATCTTCGGTTA 62
|||||

RESULT 9
US-10-479-674-27/c
; Sequence 27, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479, 674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348, 042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-27

Query Match 100.0%; Score 20; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
|||||

Db 81 TTCTTTTATCTTCGGTTA 62
|||||

RESULT 10
US-10-479-674-29/c
; Sequence 29, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.

```
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 29
/ LENGTH: 744
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-29

Query Match 100.0%; Score 20; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 72 TTCTTTTATCTTCGGTTA 53

RESULT 11
US-10-479-674-28/c
/ Sequence 28, Application US/10479674
/ Publication No. US20050019893A1
/ GENERAL INFORMATION:
/ APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 28
/ LENGTH: 782
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-28

Query Match 100.0%; Score 20; DB 9; Length 782;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 80 TTCTTTTATCTTCGGTTA 61

RESULT 12
US-10-479-674-191/c
/ Sequence 191, Application US/10479674
/ Publication No. US20050019893A1
/ GENERAL INFORMATION:
/ APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 191
```

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/ LENGTH: 1858
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-191

Query Match 100.0%; Score 20; DB 9; Length 1858;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 80 TTCTTTTATCTTCGGTTA 61

RESULT 13
US-10-479-674-192/c
/ Sequence 192, Application US/10479674
/ Publication No. US20050019893A1
/ GENERAL INFORMATION:
/ APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 192
/ LENGTH: 1861
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-192

Query Match 100.0%; Score 20; DB 9; Length 1861;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 81 TTCTTTTATCTTCGGTTA 62

RESULT 14
US-10-479-674-193/c
/ Sequence 193, Application US/10479674
/ Publication No. US20050019893A1
/ GENERAL INFORMATION:
/ APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 193
/ LENGTH: 1861
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-193

Query Match 100.0%; Score 20; DB 9; Length 1861;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
```

Db 81 TTCTTTTATCTTCGGTTA 62

RESULT 15

US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostica (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match 100.0%; Score 20; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20

Db 1117 TTCTTTTATCTTCGGTTA 1098

Search completed: May 31, 2006, 23:02:15
Job time : 520.589 secs


```

; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75910
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (460)..(495)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-75910

Query Match          79.0%; Score 15.8; DB 7; Length 612;
Best Local Similarity 89.5%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTT 19
Db      539 TTATTTTATCTTCGTGTT 521

RESULT 3
US-10-953-349-10244/c
; Sequence 10244, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10244
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10244

Query Match          79.0%; Score 15.8; DB 6; Length 1794;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTT 19
Db      267 TTCTTTTAACTTCGTGTT 249

RESULT 4
US-10-953-349-12711
; Sequence 12711, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12711
; LENGTH: 1817
; TYPE: DNA
; ORGANISM: Glycine max

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US-10-953-349-12711
Query Match          79.0%; Score 15.8; DB 6; Length 1817;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TCTTTTATCTTCGGTTA 20
Db      1704 TCTTTTAGCTTCGTGTTA 1722

RESULT 5
US-11-217-529-78725/c
; Sequence 78725, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78725
; LENGTH: 2292
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78725

Query Match          79.0%; Score 15.8; DB 7; Length 2292;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTT 19
Db      1557 TTCTTTATTTCTTCGGTT 1539

RESULT 6
US-10-953-349-11714/c
; Sequence 11714, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11714
; LENGTH: 2500
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11714

Query Match          79.0%; Score 15.8; DB 6; Length 2500;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTT 19
Db      1894 TTCTTTGTTATCTTCGTGTT 1876

```

```
RESULT 7
US-10-953-349-37451/c
; Sequence 37451, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37451
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37451

Query Match          79.0%; Score 15.8; DB 6; Length 2805;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
    ||||| ||||| ||||| ||
Db 494 TTCTTTTCTCTCGATT 476

RESULT 8
US-11-239-676-2
; Sequence 2, Application US/11239676
; Publication No. US20060107348A1
; GENERAL INFORMATION:
; APPLICANT: WU, KUNSHENG
; APPLICANT: MCCLAIRD, PAUL
; APPLICANT: BYRUM, JOSEPH R.
; APPLICANT: REITER, ROBERT
; APPLICANT: ERICKSON, MARK
; TITLE OF INVENTION: HIGH YIELDING SOYBEAN PLANTS WITH LOW LINOLENIC ACID
; FILE REFERENCE: MSUT:014US
; CURRENT APPLICATION NUMBER: US/11/239,676
; CURRENT FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: 60/614,331
; PRIOR FILING DATE: 2004-09-29
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4160
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-239-676-2

Query Match          79.0%; Score 15.8; DB 7; Length 4160;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
    ||||| ||||| ||||| ||
Db 2460 TTCTTTTCTCTCGCTT 2478

RESULT 9
US-10-505-928-607/c
; Sequence 607, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
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; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 607
; LENGTH: 135090
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-607

Query Match          79.0%; Score 15.8; DB 6; Length 135090;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTTTTATCTTCGGTTA 20
    ||||| ||||| ||||| ||
Db 122446 TCTTATTATCTTCAGTTA 122428

RESULT 10
US-11-217-529-77628
; Sequence 77628, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77628
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77628

Query Match          77.0%; Score 15.4; DB 7; Length 2022;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTTTATCTTCGGTTA 20
    ||||| ||||| ||||| ||
Db 666 TTTTCTATCTTCGGTTA 682

RESULT 11
US-11-217-529-166770/c
; Sequence 166770, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 166770
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166770

Query Match      76.0%; Score 15.2; DB 7; Length 348;
Best Local Similarity 85.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 282 TTCTTTTATCTTCGGTTA 263

RESULT 12
US-11-217-529-190895/c
; Sequence 190895, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190895
; LENGTH: 743
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-190895

Query Match      76.0%; Score 15.2; DB 7; Length 743;
Best Local Similarity 85.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 674 TTCTTTTATCTTCGGTTA 655

RESULT 13
US-11-226-605-52/c
; Sequence 52, Application US/11226605
; Publication No. US20060088859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198US01
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-52

Query Match      76.0%; Score 15.2; DB 7; Length 1003;
Best Local Similarity 85.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 192 TTCTTTTATCTTCATTTA 173

RESULT 15
US-11-122-986-229/c
; Sequence 229, Application US/1122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 231
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-11-122-986-231/c

Query Match      76.0%; Score 15.2; DB 7; Length 1398;
Best Local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 192 TTCTTTTATCTTCATTTA 173

RESULT 14
US-11-122-986-231/c
; Sequence 231, Application US/1122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 231
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-11-122-986-231
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; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 229
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-11-122-986-229

Query Match      76.0%; Score 15.2; DB 7; Length 1401;
Best Local Similarity 85.0%; Pred.No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TTCTTTTTCCTTCGGTTA 20
Db      192 TTCTTTTTCCTTCATTTA 173

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Search completed: May 31, 2006, 21:22:01
Job time : 7.65432 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 44.6914 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20

Sequence: 1 tcatgtcgttaattttt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PTTUS COMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	2007	2	US-08-743-637B-169 Sequence 169, App
C 2	20	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	20	100.0	2028	3	US-09-134-001C-1710 Sequence 1710, App
C 4	18.4	92.0	601	3	US-09-949-016-23426 Sequence 23426, A
C 5	18.4	92.0	601	3	US-09-949-016-176611 Sequence 176611, A
C 6	18.4	92.0	1133	3	US-10-000-489-57 Sequence 57, Appl
C 7	18.4	92.0	1133	4	US-09-992-095B-57 Sequence 57, Appl
C 8	18.4	92.0	1133	5	US-10-000-986A-57 Sequence 57, Appl
C 9	18.4	92.0	5372	3	US-09-949-016-5039 Sequence 5039, App
C 10	18.4	92.0	5387	3	US-09-949-016-265 Sequence 265, App
C 11	18.4	92.0	55703	3	US-09-949-016-12007 Sequence 12007, A
C 12	18.4	92.0	55703	3	US-09-949-016-16781 Sequence 16781, A
C 13	18	90.0	27	2	US-08-743-637B-262 Sequence 262, App
C 14	17.4	87.0	94077	3	US-09-949-016-13635 Sequence 13635, A
C 15	17.4	87.0	264358	3	US-09-949-016-15725 Sequence 15725, A
C 16	17	85.0	330	2	US-08-437-013-4 Sequence 4, Appli
C 17	17	85.0	330	3	US-09-275-506A-4 Sequence 4, Appli
C 18	17	85.0	601	3	US-09-949-016-69828 Sequence 69828, A
C 19	17	85.0	601	3	US-09-949-016-69829 Sequence 69829, A
C 20	17	85.0	601	3	US-09-949-016-69832 Sequence 69832, A
C 21	17	85.0	601	3	US-09-949-016-96132 Sequence 96132, A
C 22	17	85.0	601	3	US-09-949-016-96133 Sequence 96133, A
C 23	17	85.0	641	2	US-08-437-013-1 Sequence 1, Appli
C 24	17	85.0	641	2	US-08-437-013-28 Sequence 28, Appli

24	17	85.0	641	3	US-09-275-506A-1	Sequence 1, Appli
25	17	85.0	641	3	US-09-275-506A-28	Sequence 28, Appl
26	17	85.0	700	3	US-09-735-271-332	Sequence 332, App
27	17	85.0	700	3	US-09-735-271-333	Sequence 333, App
28	17	85.0	709	2	US-08-437-013-26	Sequence 26, Appl
29	17	85.0	709	3	US-09-275-506A-26	Sequence 26, Appl
30	17	85.0	12690	3	US-09-949-016-13799	Sequence 13799, A
31	17	85.0	387902	3	US-09-949-016-14543	Sequence 14543, A
32	17	85.0	421883	3	US-09-949-016-12557	Sequence 12557, A
33	16.8	84.0	497	3	US-09-621-976-2000	Sequence 2000, Ap
34	16.8	84.0	601	3	US-09-949-016-67918	Sequence 67918, A
35	16.8	84.0	601	3	US-09-949-016-81047	Sequence 81047, A
36	16.8	84.0	601	3	US-09-949-016-156906	Sequence 156906, A
37	16.8	84.0	601	3	US-09-949-016-156907	Sequence 156907, A
38	16.8	84.0	601	3	US-09-949-016-166158	Sequence 166158, A
39	16.8	84.0	601	3	US-09-949-016-173357	Sequence 173357, A
40	16.8	84.0	601	3	US-09-949-016-173358	Sequence 173358, A
41	16.8	84.0	805	2	US-08-118-469A-6	Sequence 6, Appli
42	16.8	84.0	805	2	US-08-909-119-6	Sequence 6, Appli
43	16.8	84.0	805	3	US-09-152-588-6	Sequence 6, Appli
44	16.8	84.0	2119	3	US-09-240-639-7	Sequence 7, Appli
45	16.8	84.0	2119	3	US-09-908-510A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match      100.0%; Score 20; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTTT 20
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Db 1234 TCATTGCTGTTAATATTTTT 1215

RESULT 2
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match      100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTTT 20
    |||||
Db 1234 TCATTGCTGTTAATATTTTT 1215

RESULT 3
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      100.0%; Score 20; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTTT 20
    |||||
Db 1255 TCATTGCTGTTAATATTTTT 1236

RESULT 4
US-09-949-016-23426/c
; Sequence 23426, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23426
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23426

Query Match      92.0%; Score 18.4; DB 3; Length 601;
Best Local Similarity 95.0%; Pred. No. 83;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTTT 20
    |||||
Db 284 TCATTGCTGTTAATATTTTT 265

RESULT 5
US-09-949-016-176611/c
; Sequence 176611, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```



```

; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: JPatent
; SEQ ID NO 57
; LENGTH: 1133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..475
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 476..964
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 965..1133
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 1101..1106
; FEATURE:
; NAME/KEY: polyA site
; LOCATION: 1118..1133
; LOCATION: 1118..1133
US-10-000-986A-57

Query Match          92.0%; Score 18.4; DB 5; Length 1133;
Best Local Similarity 95.0%; Pred. No. 85;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1076 TAATTGCTGTTAAATATTTT 1095

RESULT 9
US-09-949-016-5039
; Sequence 5039, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5039
; LENGTH: 5372
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5039

Query Match          92.0%; Score 18.4; DB 3; Length 5372;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 5077 TAATTGCTGTTAAATATTTT 5096

RESULT 10
US-09-949-016-265
; Sequence 265, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 5387
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-265

Query Match          92.0%; Score 18.4; DB 3; Length 5387;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 5075 TAATTGCTGTTAAATATTTT 5094

RESULT 11
US-09-949-016-12007
; Sequence 12007, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12007
; LENGTH: 55703
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12007

Query Match          92.0%; Score 18.4; DB 3; Length 55703;
Best Local Similarity 95.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 53408 TAATTGCTGTTAAATATTTT 53427

RESULT 12
US-09-949-016-16781
; Sequence 16781, Application US/09949016
```

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16781
; LENGTH: 55703
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16781

Query Match          92.0%; Score 18.4; DB 3; Length 55703;
Best Local Similarity 95.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 20
      |||||||
Db      53408 TAATGCTGTTAATATTTT 53427

RESULT 13
US-08-743-637B-262
; Sequence 262, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 262:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-743-637B-262

Query Match          90.0%; Score 18; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ATTGCTGTTAATATTTT 20
      |||||||
Db      1 ATTGCTGTTAATATTTT 18

RESULT 14
US-09-949-016-13635
; Sequence 13635, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13635
; LENGTH: 94077
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13635

Query Match          87.0%; Score 17.4; DB 3; Length 94077;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATTGCTGTTAATATTTT 20
      |||||||
Db      72712 CATTGCTGTTAATATTTT 72730

RESULT 15
US-09-949-016-15725/c
; Sequence 15725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15725
; LENGTH: 264358
; TYPE: DNA
; ORGANISM: Human

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(264358)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15725

Query Match      87.0%; Score 17.4; DB 3; Length 264358;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAAATATTTT 19
Db      115919 TCATTGCTGTTAAATATTTT 115901

Search completed: May 31, 2006, 21:13:03
Job time : 45.6914 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 519.589 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20

Sequence: 1 tcattgctgtaataattttt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	20	100.0	20	3	US-09-865-579A-14		Sequence 14, Appl
2	20	100.0	20	3	US-09-865-579A-24		Sequence 24, Appl
3	20	100.0	281	10	US-10-995-051-14		Sequence 14, Appl
4	20	100.0	560	10	US-10-478-633A-151		Sequence 151, Appl
5	20	100.0	652	9	US-10-479-674-30		Sequence 30, Appl
6	20	100.0	657	9	US-10-479-674-27		Sequence 27, Appl
7	20	100.0	744	9	US-10-479-674-29		Sequence 29, Appl
8	20	100.0	782	9	US-10-479-674-28		Sequence 28, Appl
9	20	100.0	1858	9	US-10-479-674-191		Sequence 191, Appl
10	20	100.0	1861	9	US-10-479-674-192		Sequence 192, Appl
11	20	100.0	1861	9	US-10-479-674-193		Sequence 193, Appl
12	20	100.0	1957	9	US-10-479-674-82		Sequence 82, Appl
13	20	100.0	2007	3	US-09-452-599-169		Sequence 169, Appl
14	20	100.0	2007	7	US-10-121-120-169		Sequence 169, Appl
15	20	100.0	2007	9	US-10-479-674-78		Sequence 78, Appl
16	20	100.0	2007	9	US-10-479-674-90		Sequence 90, Appl
17	20	100.0	2007	9	US-10-479-674-91		Sequence 91, Appl

C 18	20	100.0	2007	9	US-10-121-120-169		Sequence 169, Appl
C 19	20	100.0	2028	8	US-10-724-972A-3141		Sequence 3141, Ap
C 20	20	100.0	2386	9	US-10-479-674-224		Sequence 224, App
C 21	20	100.0	2410	9	US-10-479-674-190		Sequence 190, App
C 22	20	100.0	2436	9	US-10-479-674-31		Sequence 31, Appl
C 23	20	100.0	3101	9	US-10-479-674-195		Sequence 195, App
C 24	20	100.0	3506	9	US-10-479-674-196		Sequence 196, App
C 25	18.4	92.0	366	4	US-09-925-065A-405159		Sequence 405159,
C 26	18.4	92.0	366	5	US-09-925-065A-405159		Sequence 405159,
C 27	18.4	92.0	648	6	US-10-001-843-114		Sequence 114, App
C 28	18.4	92.0	648	13	US-11-005-609-114		Sequence 115, App
C 29	18.4	92.0	928	6	US-10-001-843-115		Sequence 115, App
C 30	18.4	92.0	928	13	US-11-005-609-115		Sequence 115, App
C 31	18.4	92.0	1133	3	US-09-992-600A-57		Sequence 57, Appl
C 32	18.4	92.0	1133	3	US-09-924-340-57		Sequence 57, Appl
C 33	18.4	92.0	1133	3	US-09-992-095B-57		Sequence 57, Appl
C 34	18.4	92.0	1133	3	US-09-999-570-57		Sequence 57, Appl
C 35	18.4	92.0	1133	6	US-10-000-489-57		Sequence 57, Appl
C 36	18.4	92.0	1133	6	US-10-000-986-57		Sequence 57, Appl
C 37	18.4	92.0	1133	7	US-10-154-678-57		Sequence 57, Appl
C 38	18.4	92.0	1133	7	US-10-001-142-57		Sequence 57, Appl
C 39	18.4	92.0	1133	9	US-10-838-854-57		Sequence 57, Appl
C 40	18.4	92.0	1177	6	US-10-027-632-9829		Sequence 9829, Ap
C 41	18.4	92.0	1177	6	US-10-027-632-30498		Sequence 30498, A
C 42	18.4	92.0	1177	6	US-10-027-632-30499		Sequence 30499, A
C 43	18.4	92.0	1177	7	US-10-027-632-9829		Sequence 9829, Ap
C 44	18.4	92.0	1177	7	US-10-027-632-30498		Sequence 30498, A
C 45	18.4	92.0	1177	7	US-10-027-632-30499		Sequence 30499, A

ALIGNMENTS

RESULT 1

US-09-865-579A-14
; Sequence 14, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saio, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-14

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20

Db 1 TCATTGCTGTTAATATTTT 20

RESULT 2

US-09-865-579A-24
; Sequence 24, Application US/09865579A

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; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-24

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```

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCATTGCTGTTAAATATTTT 20
    |||||||
Db 1 TCATTGCTGTTAAATATTTT 20
    |||||||

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RESULT 3

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US-10-995-051-14/c
; Sequence 14, Application US/10995051
; Publication No. US20050250094A1
; GENERAL INFORMATION:
; APPLICANT: Storchoff, James
; APPLICANT: Lucas, Adam
; APPLICANT: Muller, Uwe
; APPLICANT: Bao, Yijia P
; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination
; TITLE OF INVENTION: and Scatter-Based Detection of Nanoparticle Probe Complexes
; FILE REFERENCE: MBHB-03-466-E
; CURRENT APPLICATION NUMBER: US/10/995,051
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 10/854,848
; PRIOR FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: 60/474,569
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 60/499,034
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/517,450
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: 60/567,874
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Target MecA 4 is a mecA 281 base-pair PCR amplicon.
US-10-995-051-14

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Query Match      100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 TCATTGCTGTTAAATATTTT 20
    |||||||

```

```

Db 187 TCATTGCTGTTAAATATTTT 168

```

RESULT 4

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US-10-478-633A-151/c
; Sequence 151, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent f
; TITLE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 151
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-151

```

```

Query Match      100.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TCATTGCTGTTAAATATTTT 20
    |||||||
Db 214 TCATTGCTGTTAAATATTTT 195
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```

RESULT 5

```

US-10-479-674-30/c
; Sequence 30, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIST
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-30

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```

Query Match      100.0%; Score 20; DB 9; Length 652;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCATTGCTGTTAAATATTTT 20
    |||||||
Db 148 TCATTGCTGTTAAATATTTT 129
    |||||||

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RESULT 6

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US-10-479-674-27/c
; Sequence 27, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery

```

```
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-27

Query Match      100.0%; Score 20; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
   |||||||
Db 148 TCATTGCTGTTAATATTTT 129

RESULT 7
US-10-479-674-29/c
; Sequence 29, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-29

Query Match      100.0%; Score 20; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
   |||||||
Db 139 TCATTGCTGTTAATATTTT 120

RESULT 8
US-10-479-674-28/c
; Sequence 28, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 782
; TYPE: DNA
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; ORGANISM: Staphylococcus aureus
US-10-479-674-28

Query Match      100.0%; Score 20; DB 9; Length 782;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
   |||||||
Db 147 TCATTGCTGTTAATATTTT 128

RESULT 9
US-10-479-674-191/c
; Sequence 191, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 191
; LENGTH: 1858
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-191

Query Match      100.0%; Score 20; DB 9; Length 1858;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
   |||||||
Db 147 TCATTGCTGTTAATATTTT 128

RESULT 10
US-10-479-674-192/c
; Sequence 192, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-192

Query Match      100.0%; Score 20; DB 9; Length 1861;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
   |||||||
Db 148 TCATTGCTGTTAATATTTT 129
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RESULT 11
US-10-479-674-193/c
; Sequence 193, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANCE
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-193

Query Match      100.0%; Score 20; DB 9; Length 1861;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATAATATTTT 20
DB 148 TCATTGCTGTTAATAATATTTT 129

RESULT 12
US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANCE
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 20; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATAATATTTT 20
DB 1184 TCATTGCTGTTAATAATATTTT 1165

RESULT 13
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US2002005101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; FILE REFERENCE: TV/12287.92

```

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; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATAATATTTT 20
DB 1234 TCATTGCTGTTAATAATATTTT 1215

RESULT 14
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 20; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATAATATTTT 20
DB 1234 TCATTGCTGTTAATAATATTTT 1215

RESULT 15
US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANCE
; FILE REFERENCE: TV/12287.92

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; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78
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Query Match      100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TCATTGCTGTTAATATTTT 20
        |||||||
Db      1234 TCATTGCTGTTAATATTTT 1215
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Search completed: May 31, 2006, 23:02:17
Job time : 519.589 secs
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 7.65432 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-24
Perfect score: 20
Sequence: 1 tcattgctgtaataattttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB_seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB_seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB_seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB_seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB_seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB_seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.4	87.0	4881	7	US-11-217-529-286
C 2	16.8	84.0	555	7	US-11-217-529-174434
C 3	16.8	84.0	1728	7	US-11-217-529-1190
C 4	16.8	84.0	2163	7	US-11-217-529-78062
C 5	16.8	84.0	2370	7	US-11-217-529-1315
C 6	16.8	84.0	3891	7	US-11-217-529-1874
C 7	15.8	79.0	2411	7	US-11-293-697-994
C 8	15.8	79.0	5003	6	US-10-473-173-112
C 9	15.8	79.0	394191	6	US-10-506-549-3
C 10	15.4	77.0	444	7	US-11-328-747-3
C 11	15.4	77.0	885	7	US-11-217-529-3736
C 12	15.4	77.0	2082	7	US-11-293-697-698
C 13	15.4	77.0	3547	7	US-11-293-697-1247
C 14	15.2	76.0	1101	7	US-11-217-529-75496
C 15	15.2	76.0	1122	7	US-11-217-529-78201
C 16	15.2	76.0	1124	6	US-10-953-349-7279
C 17	15.2	76.0	1308	6	US-10-504-120-14
C 18	15.2	76.0	1488	7	US-11-217-529-79270
C 19	15.2	76.0	1566	7	US-11-217-529-76326
C 20	15.2	76.0	1567	7	US-11-217-529-79711
C 21	15.2	76.0	1827	7	US-11-217-529-82557
C 22	15.2	76.0	1938	7	US-11-217-529-3079
C 23	15.2	76.0	2127	7	US-11-217-529-2653
C 24	15.2	76.0	2370	7	US-11-217-529-77236
C 25	15.2	76.0	3190	7	US-11-293-697-323

C 26	15.2	76.0	3675	7	US-11-217-529-79669	Sequence 79669, A
C 27	15.2	76.0	3756	7	US-11-217-529-77878	Sequence 77878, A
C 28	15.2	76.0	3915	7	US-11-217-529-4858	Sequence 4858, Ap
C 29	15.2	76.0	4218	7	US-11-217-529-75740	Sequence 75740, A
C 30	15	75.0	1340	6	US-10-953-349-2052	Sequence 2052, Ap
C 31	14.8	74.0	460	7	US-11-134-445-4	Sequence 4, Appli
C 32	14.8	74.0	462	7	US-11-134-445-42	Sequence 42, Appli
C 33	14.8	74.0	1233	7	US-11-217-529-76781	Sequence 76781, A
C 34	14.8	74.0	1242	7	US-11-217-529-80870	Sequence 80870, A
C 35	14.8	74.0	1359	7	US-11-217-529-75588	Sequence 75588, A
C 36	14.8	74.0	1404	7	US-11-217-529-190888	Sequence 190888, A
C 37	14.8	74.0	1564	6	US-10-953-349-4201	Sequence 4201, Ap
C 38	14.8	74.0	1611	7	US-11-217-529-2851	Sequence 2851, Ap
C 39	14.8	74.0	2286	7	US-11-293-697-230	Sequence 230, App
C 40	14.8	74.0	2660	7	US-11-293-697-801	Sequence 801, App
C 41	14.8	74.0	3054	6	US-10-528-032-12	Sequence 12, Appli
C 42	14.8	74.0	6809	6	US-10-713-648A-24	Sequence 24, Appli
C 43	14.8	74.0	70665	6	US-10-505-928-596	Sequence 596, App
C 44	14.8	74.0	394191	6	US-10-506-549-3	Sequence 3, Appli
C 45	14.4	72.0	1140	7	US-11-217-529-6176	Sequence 6176, Ap

ALIGNMENTS

RESULT 1

US-11-217-529-286/c
; Sequence 286, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 286
; LENGTH: 4881
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-286

Query Match 87.0%; Score 17.4; DB 7; Length 4881;
Best Local Similarity 94.7%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATTGCTGTTAATATTTT 20
DB 4702 CATTGCTGTTAATATTTT 4684

RESULT 2

US-11-217-529-174434/c
; Sequence 174434, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17434
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-17434

Query Match      84.0%; Score 16.8; DB 7; Length 555;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 338 TCATTGTTGTTAAATATTATT 319

RESULT 3
US-11-217-529-1190/c
; Sequence 1190, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1190
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1190

Query Match      84.0%; Score 16.8; DB 7; Length 1728;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1016 TCATTGATGTTAAATATTTT 997

RESULT 4
US-11-217-529-78062/c
; Sequence 78062, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1190
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1190

Query Match      84.0%; Score 16.8; DB 7; Length 1728;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1016 TCATTGATGTTAAATATTTT 997

RESULT 5
US-11-217-529-1315/c
; Sequence 1315, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1315
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1315

Query Match      84.0%; Score 16.8; DB 7; Length 2370;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1504 TCATTGCTGTTACTATTTCT 1485

RESULT 6
US-11-217-529-1874/c
; Sequence 1874, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1874
; LENGTH: 3891
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1874
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Query Match 84.0%; Score 16.8; DB 7; Length 3891;
Best Local Similarity 90.0%; Pred. NO. 27;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCATTGCTGTTAATAATTTT 20
Db 3509 TTATTGTTGTTAATAATTTT 3490

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RESULT 7
US-11-293-697-994
; Sequence 994, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 994
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-994

```

Qy 2 CATTGCTGTTAATAATTTT 20
Db 2267 CATTGCTGTTGATACATTTT 2285

```

RESULT 8
US-10-473-173-112/c
; Sequence 112, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 112
; LENGTH: 5003
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-112

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QY 2 CATTGCTGTTAATATTTT 20
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D6 2862 CATTGCTGTCAATAATTTT 2844

RESULT 9
US-10-506-549-3
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1

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: GENERAL INFORMATION:
: APPLICANT: APPLERA CORPORATION
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CL001361-US
: CURRENT APPLICATION NUMBER: US/10/506,549
: CURRENT FILING DATE: 2004-09-03
: PRIOR APPLICATION NUMBER: 60/361,343
: PRIOR FILING DATE: 2002-03-05
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 394191
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(394191)
: OTHER INFORMATION: n = A,T,C or G
: US-10-506-549--3

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Qy 2 CATTCGTGTTAATATTTT 20
222820 CATTCGTGTTATCTTTT 222838
Db

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RESULT 10
US-11-328-747-3/c
; Sequence 3, Application US/11328747
; Publication No. US20060105409A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigal Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/11/328,747
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/835,096
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: E2 Ubc5c
US-11-328-747-3

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Qy 2 CATGCTGTTAAATTTT 18
Db 244 CATTACTGTTAAATTTT 228

RESULT 11
US-11-217-529-3736/c
; Sequence 3736, Application US/11217529

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; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3736
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3736

Query Match      77.0%; Score 15.4; DB 7; Length 885;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TTGCTGTTAAATATTTT 20
        |||||
Db      164 TTGCTGTTAAATATCTT 148
        |||||

RESULT 12
US-11-293-697-698
; Sequence 698, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 698
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-698

Query Match      77.0%; Score 15.4; DB 7; Length 2082;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATTGCTGTTAAATATTTT 19
        |||||
Db      1746 ATTGCTGTTAAATATTTT 1762
        |||||

RESULT 13
US-11-293-697-1247
; Sequence 1247, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; ORGANISM: Saccharomyces pastorianus

US-11-217-529-75496/c
; Sequence 75496, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75496
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75496

Query Match      76.0%; Score 15.2; DB 7; Length 1101;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAAATATTTT 20
        |||||
Db      542 TCATTGCTGTTGACATATT 523
        |||||

RESULT 15
US-11-217-529-78201/c
; Sequence 78201, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78201
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
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US-11-217-529-78201

Query Match 76.0%; Score 15.2; DB 7; Length 1122;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCATTGCTGTTAATATTTT 20
| | | | | | | | | | | | | | | | | | | | |
Db 197 TCATTGCTATTATTAATT 178

Search completed: May 31, 2006, 21:22:04
Job time : 8.65432 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 62.5679 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28
Sequence: 1 caactaactattgctaaagtccaaa 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	108	3	US-09-109-329-13
2	28	100.0	2007	2	US-08-743-637B-169
3	28	100.0	2007	3	US-08-526-840B-169
4	28	100.0	2028	3	US-09-134-001C-1710
5	25	89.3	89	3	US-09-109-329-4
6	20.6	73.6	270	3	US-09-107-433-379
7	20.6	73.6	13206	3	US-08-961-527-33
8	20.6	73.6	16995	3	US-08-961-527-82
9	20	71.4	106450	3	US-09-949-016-13873
10	19.2	68.6	516	3	US-09-621-976-2398
11	19	67.9	192	3	US-09-107-433-313
12	19	67.9	270	3	US-09-107-433-311
13	19	67.9	276	3	US-09-583-110-245
14	19	67.9	300	3	US-09-107-433-988
15	19	67.9	537	3	US-09-583-110-1340
16	19	67.9	573	3	US-09-583-110-19
17	19	67.9	573	3	US-09-583-110-598
18	19	67.9	573	3	US-09-583-110-599
19	19	67.9	573	3	US-09-583-110-620
20	19	67.9	573	3	US-09-583-110-1285
21	19	67.9	573	3	US-09-583-110-2541
22	19	67.9	573	3	US-09-107-433-312
23	19	67.9	597	3	US-09-107-433-1465

c	24	19	67.9	747	3	US-09-601-198-138	Sequence 138, App
c	25	19	67.9	1305	3	US-09-543-681A-2094	Sequence 2094, Ap
c	26	19	67.9	1635	3	US-09-601-198-10	Sequence 10, Appl
c	27	19	67.9	2996	3	US-08-961-527-260	Sequence 260, App
c	28	19	67.9	11309	3	US-08-961-527-108	Sequence 108, App
c	29	19	67.9	134499	4	US-09-531-120-192	Sequence 192, App
c	30	18.6	66.4	226	3	US-09-235-451-40	Sequence 40, Appl
c	31	18.6	66.4	226	3	US-09-978-303-40	Sequence 40, Appl
c	32	18.6	66.4	11443	3	US-08-961-527-49	Sequence 49, Appl
c	33	18.6	66.4	51336	3	US-09-949-016-16054	Sequence 16054, A
c	34	18.4	65.7	468	3	US-09-543-681A-1990	Sequence 1990, Ap
c	35	18.4	65.7	601	3	US-09-949-016-195930	Sequence 195930, A
c	36	18.4	65.7	741	3	US-09-328-352-2187	Sequence 2187, Ap
c	37	18.4	65.7	903	3	US-09-248-796A-254	Sequence 254, App
c	38	18.4	65.7	147321	3	US-09-949-016-15450	Sequence 15450, A
c	39	18.4	65.7	251672	3	US-09-949-016-17296	Sequence 17296, A
c	40	18.4	65.7	251682	3	US-09-949-016-11973	Sequence 11973, A
c	41	18.2	65.0	601	3	US-09-949-016-42368	Sequence 42368, A
c	42	18.2	65.0	601	3	US-09-949-016-42369	Sequence 42369, A
c	43	18.2	65.0	11811	3	US-09-949-016-15776	Sequence 15776, A
c	44	18.2	65.0	18122	3	US-09-949-016-12956	Sequence 12956, A
c	45	18.2	65.0	237241	3	US-09-949-016-16101	Sequence 16101, A

ALIGNMENTS

RESULT 1

US-09-109-329-13
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA gene from Staphylococcal Species

US-09-109-329-13

Query Match 100.0%; Score 28; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACAACTATTGATGCTAAAGTCAAA 28
|||
Db 67 CAACAACTATTGATGCTAAAGTCAAA 94

RESULT 2

US-08-743-637B-169
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

```
;
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-743-637B-169

Query Match 100.0%; Score 28; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACCTAACTATTGATGCTAAAGTTCAAA 28
Db 973 CAACCTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 3
US-08-526-840B-169
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACCTAACTATTGATGCTAAAGTTCAAA 28
Db 973 CAACCTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 4
US-09-134-001C-1710
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
; US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACCTAACTATTGATGCTAAAGTTCAAA 28
Db 994 CAACCTAACTATTGATGCTAAAGTTCAAA 1021

RESULT 5
US-09-109-329-4/c
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; TITLE OF INVENTION: STAPHYLOCOCCI
```

```
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-4

Query Match      89.3%; Score 25; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAACTATTGATGCTAAAGTTC 25
Db 25 CAACAACTATTGATGCTAAAGTTC 1

RESULT 6
US-09-107-433-379
; Sequence 379, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...270
; SEQUENCE DESCRIPTION: SEQ ID NO: 379:
US-09-107-433-379

Query Match      73.6%; Score 20.6; DB 3; Length 270;
Best Local Similarity 85.2%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTAAAGTTCAAA 28
Db 62 AACTAACTATTGATGATAAAGTTCAGA 88

RESULT 7
US-08-961-527-33/c
; Sequence 33, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-33

Query Match      73.6%; Score 20.6; DB 3; Length 13206;
Best Local Similarity 85.2%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTAAAGTTCAAA 28
Db 777 AACTAACTATTGATGATAAAGTTCAGA 751

RESULT 8
US-08-961-527-82/c
; Sequence 82, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16995 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-82

Query Match 73.6%; Score 20.6; DB 3; Length 16995;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAATTGCTGCTAAAGTTCAA 28
DB 456 AACTAATTGCTGCTAAAGTTCAA 430

RESULT 9
US-09-949-016-13873/c
; Sequence 13873, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13873
; LENGTH: 106450
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13873

Query Match 71.4%; Score 20; DB 3; Length 106450;
Best Local Similarity 82.1%; Pred. No. 48;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACTAATTGCTGCTAAAGTTCAA 28

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DB 71484 CTACTAAGTGTGCTGCTAAATTCAAA 71457

RESULT 10
US-09-621-976-2388
; Sequence 2388, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2388
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 78..308
; US-09-621-976-2388

Query Match 68.6%; Score 19.2; DB 3; Length 516;
Best Local Similarity 87.5%; Pred. No. 66;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTAACATTGCTGCTAAAGTTCAA 27
DB 347 CTAACATTGCTGCTAAAGTTGAA 370

RESULT 11
US-09-107-433-313
; Sequence 313, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <unknown>
; OPERATING SYSTEM: <unknown>
; SOFTWARE: <unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277

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Job time : 63.5679 secs

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 988:

SEQUENCE CHARACTERISTICS:

LENGTH: 300 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...300

SEQUENCE DESCRIPTION: SEQ ID NO: 988:

US-09-107-433-988

Query Match 67.9%; Score 19; DB 3; Length 300;
Best Local Similarity 81.5%; Pred. No. 77;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTAAAGTTCAAA 28

DB 92 AATTAACCTATGATGATAAAGTTCAGA 118

RESULT 15

US-09-583-110-1340

; Sequence 1340, Application US/09583110

; Patent No. 6699703

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.

; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

; FILE REFERENCE: PATH00-07A

; CURRENT APPLICATION NUMBER: US/09/583,110

; CURRENT FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/107,433

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/085,131

; PRIOR FILING DATE: 1998-05-12

; PRIOR APPLICATION NUMBER: US 60/051,553

; PRIOR FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 5322

; SEQ ID NO 1340

; LENGTH: 537

; TYPE: DNA

; ORGANISM: Streptococcus pneumoniae

US-09-583-110-1340

Query Match 67.9%; Score 19; DB 3; Length 537;
Best Local Similarity 81.5%; Pred. No. 81;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTAAAGTTCAAA 28

DB 5 AATTAACCTATGATGATAAAGTTCAGA 31

Search completed: May 31, 2006, 21:13:05

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: May 31, 2006, 21:16:53 ; Search time 727.424 Seconds
 (without alignments)
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 Title: US-09-865-579A-25
 Perfect score: 28
 Sequence: 1 caactaactattgatgctaaagtccaaa 28
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 18992170 seqs, 6143817638 residues
 Total number of hits satisfying chosen parameters: 37784340
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA Main:*

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2:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
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8:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
9:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
10:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
11:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
12:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
13:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
14:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
15:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
16:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28	100.0	28	3	US-09-865-579A-25	Sequence 25, Appl
2	28	100.0	28	7	US-10-382-328-1	Sequence 1, Appl
3	28	100.0	1957	3	US-10-479-674-82	Sequence 82, Appl
4	28	100.0	2007	3	US-09-452-599-169	Sequence 169, Appl
5	28	100.0	2007	7	US-10-121-120-169	Sequence 169, Appl
6	28	100.0	2007	9	US-10-479-674-78	Sequence 78, Appl
7	28	100.0	2007	9	US-10-479-674-90	Sequence 90, Appl
8	28	100.0	2007	9	US-10-479-674-91	Sequence 91, Appl
9	28	100.0	2007	9	US-10-121-120-169	Sequence 169, Appl
10	28	100.0	2028	8	US-10-724-972A-3141	Sequence 3141, Appl
11	22.2	79.3	1163020	8	US-10-398-221-10	Sequence 10, Appl
12	22.2	79.3	3011208	8	US-10-398-221-2058	Sequence 2058, Appl
13	20.6	73.6	252	9	US-10-472-928-4935	Sequence 4935, Appl
14	20.6	73.6	270	10	US-10-617-320-379	Sequence 379, Appl
15	20.6	73.6	507	9	US-10-472-928-625	Sequence 625, Appl
16	20.6	73.6	13206	2	US-08-961-527-33	Sequence 33, Appl
17	20.6	73.6	13206	8	US-10-158-844-82	Sequence 82, Appl

c 18	20.6	73.6	16995	2	US-08-961-527-82	Sequence 82, Appl
c 19	20.6	73.6	16995	8	US-10-158-844-82	Sequence 82, Appl
c 20	20.6	73.6	2162598	9	US-10-472-928-4935	Sequence 4935, Appl
c 21	20.2	72.1	477	8	US-10-424-599-78315	Sequence 78315, A
c 22	20	71.4	522	12	US-10-301-480-72989	Sequence 72989, A
c 23	20	71.4	522	12	US-10-301-480-686398	Sequence 686398, A
c 24	20	71.4	546	6	US-10-027-632-231114	Sequence 231114, A
c 25	20	71.4	546	6	US-10-027-632-231115	Sequence 231115, A
c 26	20	71.4	546	7	US-10-027-632-231114	Sequence 231114, A
c 27	20	71.4	546	7	US-10-027-632-231115	Sequence 231115, A
c 28	20	71.4	612	5	US-09-925-065A-900768	Sequence 900768, A
c 29	20	71.4	612	5	US-09-925-065A-900768	Sequence 900768, A
c 30	20	71.4	644	4	US-09-925-065A-904307	Sequence 904307, A
c 31	20	71.4	644	5	US-09-925-065A-904307	Sequence 904307, A
c 32	19.6	70.0	532	12	US-10-301-480-268574	Sequence 268574, A
c 33	19.6	70.0	532	12	US-10-301-480-861983	Sequence 861983, A
c 34	19.6	70.0	538	4	US-09-925-065A-177463	Sequence 177463, A
c 35	19.6	70.0	538	5	US-09-925-065A-177463	Sequence 177463, A
c 36	19.6	70.0	577	4	US-09-925-065A-177464	Sequence 177464, A
c 37	19.6	70.0	577	5	US-09-925-065A-177464	Sequence 177464, A
c 38	19.6	70.0	588	12	US-10-301-480-268575	Sequence 268575, A
c 39	19.6	70.0	588	12	US-10-301-480-861984	Sequence 861984, A
c 40	19.2	68.6	491	3	US-09-560-863-992	Sequence 992, App
c 41	19.2	68.6	532	4	US-09-925-065A-844656	Sequence 844656, App
c 42	19.2	68.6	532	5	US-09-925-065A-844656	Sequence 844656, App
c 43	19	67.9	192	10	US-10-617-320-313	Sequence 313, App
c 44	19	67.9	270	10	US-10-617-320-311	Sequence 311, App
c 45	19	67.9	300	10	US-10-617-320-988	Sequence 988, App

ALIGNMENTS

RESULT 1

US-09-865-579A-25
 ; Sequence 25, Application US/09865579A
 ; Patent No. US20020098492A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Taya, Toshiki
 ; APPLICANT: Ishiguro, Takahiko
 ; APPLICANT: Saito, Juichi
 ; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
 ; CURRENT FILING DATE: 2001-05-29
 ; FILE REFERENCE: 9558-003-27
 ; CURRENT APPLICATION NUMBER: US/09/865,579A
 ; PRIOR FILING DATE: 2000-05-29
 ; PRIOR APPLICATION NUMBER: JP 2000-163149
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: JP 2000-179394
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 25
 ; LENGTH: 28
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-09-865-579A-25

Query Match 100.0%; Score 28; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0

QY 1 CAACAACTATTGATGCTAAAGTTCAAA 28
 |||||
 DB 1 CAACAACTATTGATGCTAAAGTTCAAA 28
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RESULT 2

US-10-382-328-1
 ; Sequence 1, Application US/10382328
 ; Publication No. US20030219729A1

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; GENERAL INFORMATION:
; APPLICANT: YASUKAWA, Kiyoshi
; TITLE OF INVENTION: UNARY AVIAN MYELOBLASTOSIS VIRUS REVERS TRANSCRIPTASE AND ITS USE
; FILE REFERENCE: Q74425
; CURRENT APPLICATION NUMBER: US/10/382,328
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: JP 2002-071841
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-382-328-1

Query Match      100.0%; Score 28; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
   |||||
DB 1 CAACTAACTATTGATGCTAAAGTTCAAA 28

RESULT 3
US-10-479-674-82
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infetio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 28; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
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DB 923 CAACTAACTATTGATGCTAAAGTTCAAA 950

RESULT 4
US-09-452-599-169
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
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; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
   |||||
DB 973 CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 5
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 28; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
   |||||
DB 973 CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 6
US-10-479-674-78
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infetio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIS
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
Db 973 CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 7
US-10-479-674-90
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
Db 973 CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 8
US-10-479-674-91
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
Db 973 CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 9
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
Db 973 CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 10
US-10-724-972A-3141
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match      100.0%; Score 28; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CAACTAACTATTGATGCTTAAAGTTCAA 28
|||||
Db 994 CAACTAACTATTGATGCTTAAAGTTCAA 1021

RESULT 11

US-10-398-221-10/c
; Sequence 10, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1163020
; TYPE: DNA
; ORGANISM: Listeria innocua
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u

US-10-398-221-10

Query Match 79.3%; Score 22.2; DB 8; Length 1163020;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTTAAAGTTCAA 28
|||||
Db 391866 AACTAACTATTGATGCTTAAAGTTCAA 391840

RESULT 12

US-10-398-221-2058/c
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2058
; LENGTH: 3011208
; TYPE: DNA
; ORGANISM: Listeria innocua

US-10-398-221-2058

Query Match 79.3%; Score 22.2; DB 8; Length 3011208;
Best Local Similarity 88.9%; Pred. No. 4.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTTAAAGTTCAA 28
|||||
Db 482132 AACTAACTATTGATGCTTAAAGTTCAA 482106

RESULT 13

US-10-472-928-4935
; Sequence 4935, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4935
; LENGTH: 252
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae

US-10-472-928-4935

Query Match 73.6%; Score 20.6; DB 9; Length 252;
Best Local Similarity 85.2%; Pred. No. 3.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTTAAAGTTCAA 28
|||||
Db 5 AACTAACTATTGATGCTTAAAGTTCAA 31

RESULT 14

US-10-617-320-379
; Sequence 379, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 379:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...270
; SEQUENCE DESCRIPTION: SEQ ID NO: 379:
US-10-617-320-379

Query Match 73.6%; Score 20.6; DB 10; Length 270;
Best Local Similarity 85.2%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTAAAGTTCAA 28

Db 62 AACTAACTATTGATGCTAAAGTTCAA 88

RESULT 15
US-10-472-928-625
; Sequence 625, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: Seqwin99, version 1.03
; SEQ ID NO 625
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-472-928-625

Query Match 73.6%; Score 20.6; DB 9; Length 507;
Best Local Similarity 85.2%; Pred. No. 4.4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTAAAGTTCAA 28

Db 5 AACTAACTATTGATGCTAAAGTTCAA 31

Search completed: May 31, 2006, 23:02:24
Job time : 733.424 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 10.716 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-25
Perfect score: 28
Sequence: 1 caactaactattgatgctaaagtcca 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	67.9	975	7	US-11-217-529-6080
2	18.4	65.7	594	7	US-11-217-529-166583
3	18	64.3	1087	6	US-10-953-349-6329
4	18	64.3	2020	7	US-11-293-697-1218
5	17.4	62.1	1359	6	US-10-953-349-15694
6	17.2	61.4	661	6	US-10-488-619-2732
7	17.2	61.4	1916	6	US-10-953-349-36474
8	17	60.7	541	6	US-10-488-619-949
9	17	60.7	1650	6	US-10-953-349-6680
10	17	60.7	2832	7	US-11-217-529-5260
11	17	60.7	3309	7	US-11-217-529-78086
12	16.8	60.0	606	7	US-11-217-529-79099
13	16.8	60.0	1004	6	US-10-953-349-17520
14	16.8	60.0	1584	6	US-10-953-349-4786
15	16.8	60.0	1608	6	US-10-953-349-13583
16	16.8	60.0	1908	7	US-11-217-529-80973
17	16.8	60.0	2016	7	US-11-217-529-2923
18	16.8	60.0	3495	7	US-11-293-697-463
19	16.8	60.0	3801	7	US-11-217-529-4511
20	16.8	60.0	3860	7	US-11-266-446-67
21	16.8	60.0	151830	6	US-10-519-335-37
22	16.6	59.3	1281	6	US-10-953-349-19184
23	16.6	59.3	2057	7	US-11-217-529-1780
24	16.6	59.3	2157	7	US-11-217-529-173838
25	16.4	58.6	435	6	US-10-488-619-270

C	26	16.4	58.6	648	7	US-11-217-529-842	Sequence 842, App
	27	16.4	58.6	771	7	US-11-217-529-5368	Sequence 5368, Ap
	28	16.4	58.6	1116	7	US-11-253-300-2	Sequence 2, Appl
	29	16.4	58.6	1292	6	US-10-953-349-27804	Sequence 27804, A
	30	16.4	58.6	1440	7	US-11-217-529-78387	Sequence 78387, A
C	31	16.4	58.6	1869	7	US-11-217-529-81293	Sequence 81293, A
	32	16.4	58.6	1965	7	US-11-217-529-4505	Sequence 4505, Ap
	33	16.4	58.6	2952	6	US-10-511-937-654	Sequence 654, App
C	34	16.2	57.9	1159	7	US-11-136-524-25	Sequence 25, Appl
	35	16.2	57.9	1173	7	US-11-217-529-312	Sequence 312, App
	36	16.2	57.9	1189	6	US-10-511-937-661	Sequence 661, App
	37	16.2	57.9	1695	7	US-11-217-529-81770	Sequence 81770, A
	38	16	57.1	622	7	US-11-217-529-191090	Sequence 191090,
C	39	16	57.1	924	7	US-11-217-529-365	Sequence 365, App
	40	16	57.1	1041	7	US-11-217-529-167027	Sequence 167027, A
C	41	16	57.1	1461	6	US-10-953-349-23327	Sequence 23327, A
	42	16	57.1	1476	7	US-11-217-529-4815	Sequence 4815, Ap
	43	16	57.1	2004	7	US-11-217-529-2004	Sequence 2004, Ap
	44	16	57.1	2691	7	US-11-217-529-460	Sequence 460, App
	45	16	57.1	3201	7	US-11-217-529-76871	Sequence 76871, A

ALIGNMENTS

RESULT 1

US-11-217-529-6080
; Sequence 6080, Application US/11217529
; Publication No. US20060099612A1

; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAWA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6080
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus

Query Match 67.9%; Score 19; DB 7; Length 975;
Best Local Similarity 81.5%; Pred. No. 4.8;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CACTTAACATTATGCTTAAGTTCAA 27
DB 309 CTACTATCTATTGAACCTAAATTTCAA 335

RESULT 2

US-11-217-529-166583
; Sequence 166583, Application US/11217529
; Publication No. US20060099612A1

; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAWA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166583
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166583

Query Match 65.7%; Score 18.4; DB 7; Length 594;
Best Local Similarity 78.6%; Pred. No. 8.3;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CACTAATCTTGCCTAAAGTTCAA 28
Db 313 CAAGAAATCTTGCCTAAAGTTCAA 340

RESULT 3
US-10-953-349-6329
; Sequence 6329, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6329
; LENGTH: 1087
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6329

Query Match 64.3%; Score 18; DB 6; Length 1087;
Best Local Similarity 80.8%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 ACTAATCTTGCCTAAAGTTCAA 28
Db 910 ACTAATCTTGCCTAAAGTTCAA 935

RESULT 4
US-11-293-697-1218
; Sequence 1218, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1218
; LENGTH: 2020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1218

Query Match 64.3%; Score 18; DB 7; Length 2020;
Best Local Similarity 80.8%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 ACTAATCTTGCCTAAAGTTCAA 28

Db 1849 ACTAATATAGATGCAAAAGTCAAA 1874
RESULT 5
US-10-953-349-15694/c
; Sequence 15694, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15694
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-15694

Query Match 62.1%; Score 17.4; DB 6; Length 1359;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 AACTAATCTTGCCTAAAGTTCAA 28
Db 854 AACAAACGCTTGAAGCAAAAGTTGAAA 828

RESULT 6
US-10-488-619-2732
; Sequence 2732, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations, and Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2732
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2732

Query Match 61.4%; Score 17.2; DB 6; Length 661;
Best Local Similarity 86.4%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 ACTATTGATGCTAAAGTTCAA 28
Db 76 ACTAATGATGCTGAAGTTCCAA 97

RESULT 7
US-10-953-349-36474/c
; Sequence 36474, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 36474
; LENGTH: 1916
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1883)..(1883)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-36474

Query Match      61.4%; Score 17.2; DB 6; Length 1916;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAG 22
    ||||| ||||| ||||| |||||
Db 1728 CAACTACTATTGAGGCTAAAG 1707

RESULT 8
US-10-488-619-949
; Sequence 949, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 949
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-949

Query Match      60.7%; Score 17; DB 6; Length 541;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ACTAACTATTGATGCTAAAGTTCAA 27
    ||||| ||||| ||||| |||||
Db 35 ACTAAATATTTCATGTTAAATTTCAA 59

RESULT 9
US-10-953-349-6680
; Sequence 6680, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6680
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6680

Query Match      60.7%; Score 17; DB 6; Length 1650;
Best Local Similarity 80.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ACTAACTATTGATGCTAAAGTTCAA 27
    ||||| ||||| ||||| |||||
Db 561 ACTTAAATTGCTTCTAAAGGTTCAA 585
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RESULT 10
US-11-217-529-5260
; Sequence 5260, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5260
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5260

Query Match      60.7%; Score 17; DB 7; Length 2832;
Best Local Similarity 80.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 3 ACTAACTATTGATGCTAAAGTTCAA 27
    ||||| ||||| ||||| |||||
Db 798 ACCAACTACTACGCTAAATTCAA 822
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RESULT 11
US-11-217-529-78086
; Sequence 78086, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78086
; LENGTH: 3309
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78086
```

```
Query Match      60.7%; Score 17; DB 7; Length 3309;
Best Local Similarity 80.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
QY 2 ACTAACTATTGATGCTAAAGTTCA 26
    ||||| ||||| ||||| |||||
Db 1634 AAATAACTTTGATTTCTAAAGTTCA 1658
```

```
RESULT 12
US-11-217-529-79099
; Sequence 79099, Application US/11217529
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; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79099
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79099

Query Match          60.0%; Score 16.8; DB 7; Length 606;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
||| ||| ||| ||| ||| ||| ||| |||
Db 322 CAAGAAATCTTTGACGCTAACGTTCAA 349

RESULT 13
US-10-953-349-17520
; Sequence 17520, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17520
; LENGTH: 1004
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17520

Query Match          60.0%; Score 16.8; DB 6; Length 1004;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 8 CTATTGATGCTAAAGTTCAA 27
||| ||| ||| ||| ||| ||| |||
Db 398 CTTTGATCTCTAAAGTTCAA 417

RESULT 14
US-10-953-349-4786
; Sequence 4786, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4786
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; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4786

Query Match          60.0%; Score 16.8; DB 6; Length 1584;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
||| ||| ||| ||| ||| ||| ||| |||
Db 344 CAACTTCTCTCGAAGCTATAGTTCACA 371

RESULT 15
US-10-953-349-13583
; Sequence 13583, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE:
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13583
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-13583

Query Match          60.0%; Score 16.8; DB 6; Length 1608;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
||| ||| ||| ||| ||| ||| ||| |||
Db 1204 CATCTACCAATTTGGTGCTGAATTTGAAA 1231

Search completed: May 31, 2006, 21:22:04
Job time : 10.716 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 87.1481 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-26
Perfect score: 39
Sequence: 1 cccaatttgatccattgttggtgatattatagcttcaga 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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8: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	39	100.0	2007	2	US-08-743-637B-169 Sequence 169, App
C 2	39	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	28	71.8	2028	3	US-09-134-001C-1710 Sequence 1710, App
C 4	23.2	59.5	11652	3	US-09-949-016-13413 Sequence 13413, A
5	22.6	57.9	2363	3	US-10-104-047-203 Sequence 203, App
6	22.4	57.4	4853	3	US-08-881-450A-22 Sequence 22, Appl
7	22	56.4	563	3	US-09-621-976-1244 Sequence 1244, App
C 8	22	56.4	601	3	US-09-949-016-18896 Sequence 18896, A
C 9	22	56.4	601	3	US-09-949-016-56872 Sequence 56872, A
C 10	22	56.4	63591	3	US-09-949-016-11808 Sequence 11808, A
C 11	22	56.4	63591	3	US-09-949-016-13388 Sequence 13388, A
C 12	21.8	55.9	1451	3	US-09-465-558-37 Sequence 37, Appl
C 13	21.6	55.4	601	3	US-09-949-016-135878 Sequence 135878, A
C 14	21.6	55.4	601	3	US-09-949-016-135995 Sequence 135995, A
C 15	21.6	55.4	601	3	US-09-949-016-136112 Sequence 136112, A
16	21.6	55.4	193555	3	US-09-949-016-15553 Sequence 15553, A
17	21.6	55.4	193555	3	US-09-949-016-15554 Sequence 15554, A
18	21.6	55.4	193555	3	US-09-949-016-15555 Sequence 15555, A
19	21.4	54.9	126153	3	US-09-949-002-596 Sequence 596, App
20	21.4	54.9	135687	3	US-09-949-002-805 Sequence 805, App
21	21.4	54.9	818128	3	US-09-949-016-14546 Sequence 14546, A
22	21.4	54.9	818128	3	US-09-949-016-14547 Sequence 14547, A
23	21.4	54.9	818128	3	US-09-949-016-14548 Sequence 14548, A

24	21.4	54.9	818128	3	US-09-949-016-14549 Sequence 14549, A
25	21.4	54.9	818128	3	US-09-949-016-14550 Sequence 14550, A
26	21.4	54.9	818128	3	US-09-949-016-14551 Sequence 14551, A
27	21.4	54.9	818128	3	US-09-949-016-14552 Sequence 14552, A
28	21.4	54.9	818128	3	US-09-949-016-14553 Sequence 14553, A
29	21.4	54.9	818128	3	US-09-949-016-14554 Sequence 14554, A
30	21.4	54.9	818128	3	US-09-949-016-14555 Sequence 14555, A
31	21.4	54.9	818128	3	US-09-949-016-14556 Sequence 14556, A
32	21.4	54.9	818128	3	US-09-949-016-14557 Sequence 14557, A
33	21.4	54.9	818128	3	US-09-949-016-14558 Sequence 14558, A
34	21.4	54.9	818128	3	US-09-949-016-14559 Sequence 14559, A
35	21.4	54.9	818128	3	US-09-949-016-14560 Sequence 14560, A
36	21.4	54.9	818128	3	US-09-949-016-14561 Sequence 14561, A
37	21.4	54.9	818128	3	US-09-949-016-14562 Sequence 14562, A
38	21.4	54.9	818128	3	US-09-949-016-14564 Sequence 14564, A
39	21.4	54.9	818128	3	US-09-949-016-14565 Sequence 14565, A
40	21.4	54.9	818128	3	US-09-949-016-14566 Sequence 14566, A
41	21.4	54.9	818128	3	US-09-949-016-14567 Sequence 14567, A
C 42	21.2	54.4	729	3	US-09-248-796A-715 Sequence 715, App
43	21.2	54.4	740	3	US-09-721-341-10 Sequence 10, Appl
44	21.2	54.4	740	3	US-09-721-495B-10 Sequence 10, Appl
45	21.2	54.4	740	4	US-09-721-341-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

```

; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match      100.0%; Score 39; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
    |||||
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 2
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match      100.0%; Score 39; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
    |||||
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

```

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; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      71.8%; Score 28; DB 3; Length 2028;
Best Local Similarity 97.5%; Pred. No. 0.58;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCATTGTTG-TTGATATAGTCTTCAGA 39
    |||||
Db 637 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 598

RESULT 4
US-09-949-016-13413/c
; Sequence 13413, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13413
; LENGTH: 116652
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(116652)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13413

Query Match      59.5%; Score 23.2; DB 3; Length 116652;
Best Local Similarity 77.8%; Pred. No. 57;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CAATTTTGATCCATTGTTGTTGATATAGTCTTCAG 38
    |||||
Db 94872 CAATCTTGCTACATTGTTGTTGATATAGTCTTCAG 94837

RESULT 5
US-10-104-047-203
; Sequence 203, Application US/10104047
; Patent No. 6943241

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```

; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 2363
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-104-047-203

Query Match 57.9%; Score 22.6; DB 3; Length 2363;
Best Local Similarity 75.7%; Pred. No. 54;
Matches 28; Conservative 0; Mismatches 9; Indels 0

QY 2 CCAATTGGATCCATTGTTGTTGATATAGTCTTTCAG 38
| | | | | | | | | | | | | | | | | | | |
Db 1896 CTAATTAGATCAATTGTTGGTTGTACAGTTAAG 1932

RESULT 6
US-08-881-450A-22
; Sequence 22, Application US/08881450A
; Patent No. 6274310
; GENERAL INFORMATION:
; APPLICANT: Habener, J.F. and Stoffers, D.A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: PANCREATIC DISEASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Inc.
; STREET: One Financial Center
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,450A
; FILING DATE: June 24, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathleen M. Williams
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 11275/7823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4853 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: IPF1 gene, contig 1.
; US-08-881-450A-22

Query Match 57.4%; Score 22.4; DB 3; Length 4853;
Best Local Similarity 67.6%; Pred. No. 71;

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RESULT 9

US-09-949-016-56872/c
; Sequence 56872, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56872
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(636591)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-56872

Query Match 56.4%; Score 22; DB 3; Length 601;
Best Local Similarity 73.7%; Pred. No. 73;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCAATTTGATCCATTGTTGTGATATAGTCTTCAGA 39

Db 581 CAAATTTTAATGCAATTCAAAGTTGATATCAATTTTCATA 544

RESULT 10

US-09-949-016-11808/c
; Sequence 11808, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11808
; LENGTH: 636591
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(636591)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11808

Query Match 56.4%; Score 22; DB 3; Length 636591;
Best Local Similarity 73.7%; Pred. No. 1.9e+02;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCAATTTGATCCATTGTTGTGATATAGTCTTCAGA 39

Db 559594 CAAATTTTAATGCAATTCAAAGTTGATATCAATTTTCATA 559557

RESULT 11

US-09-949-016-13388/c
; Sequence 13388, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13388
; LENGTH: 636591
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(636591)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13388

Query Match 56.4%; Score 22; DB 3; Length 636591;
Best Local Similarity 73.7%; Pred. No. 1.9e+02;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCAATTTGATCCATTGTTGTGATATAGTCTTCAGA 39

Db 559594 CAAATTTTAATGCAATTCAAAGTTGATATCAATTTTCATA 559557

RESULT 12

US-09-465-558-37/c
; Sequence 37, Application US/09465558
; Patent No. 6436657
; GENERAL INFORMATION:
; APPLICANT: Morakinyo, Layo O.
; TITLE OF INVENTION: TETRAHYDROFOLATE METABOLIC ENZYMES
; FILE REFERENCE: BB1322 US NA
; CURRENT APPLICATION NUMBER: US/09/465,558
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: 60/112,734
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 37
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Glycine max
US-09-465-558-37

Query Match 55.9%; Score 21.8; DB 3; Length 1451;
Best Local Similarity 78.8%; Pred. No. 98;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CAAATTTGATCCATTGTTGTGATATAGTCTTT 35

Db 1409 CAAATTTTAATCCTTTTGTGCTTGAATTAATCTT 1377

; CURRENT APPLICATION NUMBER: US/0
 : CURRENT FILING DATE: 2000-04-14

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 1013.2 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-26

Perfect score: 39

Sequence: 1 cccaatttgatccattgtgtgatattcagtcctcaga 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /EMC Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 14: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 15: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
- 16: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10K_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	39	3	US-09-865-579A-8
2	39	100.0	39	3	US-09-865-579A-26
3	39	100.0	560	10	US-10-478-633A-150
4	39	100.0	2007	3	US-09-452-599-169
5	39	100.0	2007	7	US-10-121-120-169
6	39	100.0	2007	9	US-10-479-674-78
7	39	100.0	2007	9	US-10-121-120-169
8	28	71.8	1957	9	US-10-479-674-82
9	28	71.8	2007	9	US-10-479-674-90
10	28	71.8	2028	8	US-10-724-972A-3141
11	26.4	67.7	2007	9	US-10-479-674-91
12	23.2	59.5	287	9	US-10-425-115-7606
13	23.2	59.5	777	4	US-09-925-065A-938424
14	23.2	59.5	777	5	US-09-925-065A-938424
15	23	59.0	3009	13	US-11-097-143-37397
16	23	59.0	5293	13	US-11-097-143-37396
17	23	59.0	25988	13	US-11-097-143-11350

18	22.8	58.5	1511	9	US-10-363-345A-1285	Sequence 1285, Ap
19	22.8	58.5	1511	9	US-10-363-345A-1286	Sequence 1286, Ap
20	22.8	58.5	1511	10	US-10-363-483A-1285	Sequence 1285, Ap
21	22.8	58.5	1511	10	US-10-363-483A-1286	Sequence 1286, Ap
22	22.8	58.5	1641	8	US-10-424-599-13277	Sequence 13277, A
23	22.8	58.5	5424	8	US-10-437-963-78841	Sequence 78841, A
24	22.6	57.9	426	3	US-09-813-358-91	Sequence 91, Appl
25	22.6	57.9	426	3	US-09-977-279-91	Sequence 91, Appl
26	22.6	57.9	559	4	US-09-925-065A-574125	Sequence 574125, A
27	22.6	57.9	559	4	US-09-925-065A-574126	Sequence 574126, A
28	22.6	57.9	559	4	US-09-925-065A-574127	Sequence 574127, A
29	22.6	57.9	559	5	US-09-925-065A-574125	Sequence 574125, A
30	22.6	57.9	559	5	US-09-925-065A-574126	Sequence 574126, A
31	22.6	57.9	559	5	US-09-925-065A-574127	Sequence 574127, A
32	22.6	57.9	600	10	US-10-972-079-45481	Sequence 45481, A
33	22.6	57.9	647	9	US-10-425-115-65295	Sequence 65295, A
34	22.6	57.9	894	9	US-10-424-599-27147	Sequence 27147, A
35	22.6	57.9	995	12	US-10-301-480-565340	Sequence 565340, A
36	22.6	57.9	995	12	US-10-301-480-1178749	Sequence 1178749, A
37	22.6	57.9	1707	8	US-10-437-963-80249	Sequence 80249, A
38	22.6	57.9	1921	10	US-10-487-092-55	Sequence 55, Appl
39	22.6	57.9	2212	8	US-10-437-963-29786	Sequence 29786, A
40	22.6	57.9	2363	7	US-10-104-047-203	Sequence 203, App
41	22.6	57.9	2363	16	US-11-072-512-203	Sequence 203, App
42	22.6	57.9	2490	8	US-10-437-963-81142	Sequence 81142, A
43	22.6	57.9	2685	8	US-10-437-963-96408	Sequence 96408, A
44	22.6	57.9	2742	8	US-10-437-963-29787	Sequence 29787, A
45	22.6	57.9	3018	8	US-10-437-963-29785	Sequence 29785, A

ALIGNMENTS

RESULT 1

US-09-865-579A-8
; Sequence 8, Application US/09865579A
; Patent No. US2002009492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; CURRENT APPLICATION NUMBER: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-8

Query Match 100.0%; Score 39; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAATTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
DB 1 CCAATTTGATCCATTGTTGTTGATATAGTCTTCAGA 39

RESULT 2

US-09-865-579A-26
; Sequence 26, Application US/09865579A

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; Patent No. US20020098492A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
;
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of meca Gene of
; Methicillin Resistant Staphylococcus Aureus
;
; FILE REFERENCE: 9558-003-27
;
; CURRENT APPLICATION NUMBER: US/09/865,579A
;
; CURRENT FILING DATE: 2001-05-29
;
; PRIOR APPLICATION NUMBER: JP 2000-163149
;
; PRIOR FILING DATE: 2000-05-29
;
; PRIOR APPLICATION NUMBER: JP 2000-179394
;
; PRIOR FILING DATE: 2000-06-09
;
; NUMBER OF SEQ ID NOS: 30
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 26
;
; LENGTH: 39
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Probe
;
; US-09-865-579A-26

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Query Match      100.0%; Score 39; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCCAATTITGATCCATTGTGTTGATATAGTCTTCAGA 39
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Db 1 CCCAATTITGATCCATTGTGTTGATATAGTCTTCAGA 39
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RESULT 3
US-10-478-633A-150/c
; Sequence 150, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; TITLE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 150
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-150

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Query Match	100.0%;	Score 39;	DB 10;	Length 560;
Best Local Similarity	100.0%;	Pred. No. 0.0013;		
Matches 39:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 CCCAAATTTTGATCCATTTTGTGTTGATATAGTCTTCAGA 39
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375 CCCAAATTTTGATCCATTTTGTGTTGATATAGTCTTCAGA 337
Db

RESULT 4
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers

```

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

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Query Match	100.0%;	Score 39;	DB 3;	Length 2007;
Best Local Similarity	100.0%;	Pred. No. 0.0018;		
Matches 39; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 CCCAAATTTTGATCCCAATTTGTTGTTGATATAGTCTTCAGA 39
 |||
 615 CCCAAATTTTGATCCCAATTTGTTGTTGATATAGTCTTCAGA 577
 |||

RESULT 5
 US-10-121-120-169/c
 ; Sequence 169, Application US/10121120
 ; Publication No. US20030180733A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bergeron, Michel G.
 ; APPLICANT: Ouellette, Marc
 ; APPLICANT: Roy, Paul H.
 ; TITLE OF INVENTION: Specific and Universal Probes and Amplification
 ; TITLE OF INVENTION: Primers
 ; TITLE OF INVENTION: To Rapidly Detect and Identify Common Bacterial
 ; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
 ; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
 ; FILE REFERENCE: 12287.31
 ; CURRENT APPLICATION NUMBER: US/10/121,120
 ; CURRENT FILING DATE: 2002-04-11
 ; PRIORITY APPLICATION NUMBER: 09/452,599
 ; PRIOR FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: 08/304,732
 ; PRIOR FILING DATE: 1994-09-12
 ; NUMBER OF SEQ ID NOS: 177
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 169
 ; LENGTH: 2007
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus aureus
 US-10-121-120-169

Query Match	100.0%;	Score 39;	DB 7;	Length 2007;
Best Local Similarity	100.0%;	Pred. No. 0.0018;		
Matches 39:	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy 1 CCCAAATTTTGGATCCATTTTGTGTTGATATAGTCTTCAGA 39
 |||||
 Db 615 CCCAAATTTTGGATCCATTTTGTGTTGATATAGTCTTCAGA 577

RESULT 6

US-10-479-674-78/c

; Sequence 78, Application US/10479674

; Publication No. US20050019893A1

; GENERAL INFORMATION:

; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.

; APPLICANT: Huletsky, Ann

; APPLICANT: Roszbach, Valery

; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIS

```
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match      100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 7
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Quелlette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 8
US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTAN
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82
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; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      71.8%; Score 28; DB 9; Length 1957;
Best Local Similarity 97.5%; Pred. No. 13;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 566 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 527

RESULT 9
US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTAN
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match      71.8%; Score 28; DB 9; Length 2007;
Best Local Similarity 97.5%; Pred. No. 13;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 616 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 10
US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
```

US-10-724-972A-3141

Query Match 71.8%; Score 28; DB 8; Length 2028;
Best Local Similarity 97.5%; Pred. No. 13;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCATTTGTTG-TTGATATAGTCTTCAGA 39
Db 637 CCCAATTTTGATCCATTTGTTGTTTGATATAGTCTTCAGA 598

RESULT 11

US-10-479-674-91/c

; Sequence 91, Application US/10479674

; Publication No. US2005001993A1

; GENERAL INFORMATION:

; APPLICANT: Inflectio Diagnostic (I.D.I.) Inc.

; APPLICANT: Huletsky, Ann

; APPLICANT: Roszbach, Valery

; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTA

; FILE REFERENCE: TV/12287.92

; CURRENT APPLICATION NUMBER: US/10/479,674

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: CA 2,348,042

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 91

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-91

Query Match 67.7%; Score 26.4; DB 9; Length 2007;

Best Local Similarity 95.0%; Pred. No. 47;

Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCATTTGTTG-TTGATATAGTCTTCAGA 39
Db 616 CCCAATTTTGATCCATTTGTTGTTTGATATAGTCTTCAGA 577

RESULT 12

US-10-425-115-7606

; Sequence 7606, Application US/10425115

; Publication No. US2004021427A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(S3222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 7606

; LENGTH: 287

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)-(287)

; OTHER INFORMATION: unsure at all n locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRF4577_106935C.1

US-10-425-115-7606

Query Match 59.5%; Score 23.2; DB 9; Length 287;

Best Local Similarity 77.8%; Pred. No. 4e+02;

Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 AATTTTGATCCATTTGTTGTTGATATAGTCTTCAGA 39
Db 125 AAGATTGATCCAGTAGGTGTTGATTATTCTTCAAA 160

RESULT 13

US-09-925-065A-938424/c

; Sequence 938424, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 938424

; LENGTH: 777

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-938424

Query Match 59.5%; Score 23.2; DB 4; Length 777;

Best Local Similarity 77.8%; Pred. No. 5e+02;

Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CAATTTTGATCCATTTGTTGTTGATATAGTCTTCAG 38
Db 465 CAATCTTGCTACATTTGTTTATAGATATAATGTCAG 430

RESULT 14

US-09-925-065A-938424/c

; Sequence 938424, Application US/09925065A

; Publication No. US20050228172A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 938424

; LENGTH: 777

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-938424

Query Match 59.5%; Score 23.2; DB 5; Length 777;

Best Local Similarity 77.8%; Pred. No. 5e+02; Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CAATTTTGATCCATTTGTTGATATAGTCTTCAG 38
|||||
Db 465 CAATCTTGCTACATTTGTTTGTAGATATAGTCCAG 430

RESULT 15

US-11-097-143-37397/c
; Sequence 37397, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37397
; LENGTH: 3009
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-37397

Query Match 59.0%; Score 23; DB 13; Length 3009;
Best Local Similarity 74.4%; Pred. No. 8.1e+02; Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTTGTTGATATAGTCTTCAGA 39
|||||
Db 2625 CGCATTTCGAGCACTTCGTTTTTGTAGATAGTCGCAAA 2587

Search completed: May 31, 2006, 23:02:25
Job time : 1013.2 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 14.9259 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-26
Perfect score: 39
Sequence: 1 cccaatttgatccattgtgttgatagcttcaga 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 5886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA New:*
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 - 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	56.4	1556	US-10-953-349-17882	Sequence 17882, A
2	20.8	53.3	1257	US-11-217-529-1620	Sequence 1620, Ap
3	20.6	52.8	1262	US-10-953-349-20828	Sequence 20828, A
C 4	20.4	52.3	678	US-11-217-529-3208	Sequence 3208, Ap
5	20.2	51.8	1361	US-10-953-349-3924	Sequence 3924, Ap
C 6	20	51.3	3075	US-11-217-529-77428	Sequence 77428, A
C 7	19.8	50.8	1000	US-11-233-726-20	Sequence 20, Appl
C 8	19.8	50.8	2089	US-10-953-349-22930	Sequence 22930, A
C 9	19.8	50.8	2772	US-11-217-529-75755	Sequence 75755, A
C 10	19.8	50.8	3230	US-11-293-697-2392	Sequence 2392, Ap
11	19.6	50.3	1794	US-11-217-529-81556	Sequence 81556, A
C 12	19.6	50.3	1871	US-10-953-349-6075	Sequence 6075, Ap
C 13	19.4	49.7	810	US-11-217-529-82386	Sequence 82386, A
C 14	19.4	49.7	2130	US-11-217-529-1784	Sequence 1784, Ap
C 15	19.4	49.7	2130	US-11-217-529-80690	Sequence 80690, A
C 16	19.4	49.7	2631	US-10-527-411-65	Sequence 65, Appl
C 17	19.4	49.7	2727	US-10-527-411-63	Sequence 63, Appl
C 18	19.4	49.7	2745	US-10-527-411-59	Sequence 59, Appl
C 19	19.4	49.7	2850	US-10-527-411-67	Sequence 67, Appl
C 20	19.4	49.7	3393	US-10-527-411-138	Sequence 138, Appl
C 21	19.4	49.7	4127	US-11-251-610-10	Sequence 10, Appl
C 22	19.2	49.2	498	US-10-953-349-6839	Sequence 6839, Ap
C 23	19.2	49.2	1698	US-11-217-529-482	Sequence 482, Appl
C 24	19.2	49.2	1759	US-10-504-120-1	Sequence 1, Appl
25	19.2	49.2	3132	US-11-217-529-77436	Sequence 77436, A

C 26	19.2	49.2	3396	7	US-11-217-529-75365	Sequence 75365, A
C 27	19	48.7	1290	7	US-11-302-678-54	Sequence 54, Appl
C 28	19	48.7	1413	7	US-11-217-529-173427	Sequence 173427, A
C 29	19	48.7	1557	7	US-11-302-678-52	Sequence 52, Appl
C 30	19	48.7	2346	7	US-11-251-610-18	Sequence 18, Appl
C 31	19	48.7	2361	7	US-11-293-697-493	Sequence 493, Appl
C 32	19	48.7	3247	7	US-11-251-610-3	Sequence 3, Appl
C 33	19	48.7	3336	7	US-11-217-529-80440	Sequence 80440, A
C 34	19	48.7	4852	6	US-10-505-928-417	Sequence 417, Appl
C 35	19	48.7	394191	6	US-10-506-549-3	Sequence 3, Appl
C 36	18.8	48.2	1336	6	US-10-953-349-24839	Sequence 24839, A
C 37	18.8	48.2	1548	7	US-11-217-529-6018	Sequence 6018, A
C 38	18.8	48.2	1656	7	US-11-217-529-79362	Sequence 79362, A
C 39	18.8	48.2	1662	6	US-10-953-349-16829	Sequence 16829, A
C 40	18.8	48.2	2476	6	US-10-501-834-211	Sequence 211, Appl
C 41	18.6	47.7	51	7	US-11-245-248-363	Sequence 363, Appl
C 42	18.6	47.7	276	7	US-11-263-326-115	Sequence 115, Appl
C 43	18.6	47.7	321	7	US-11-217-529-77583	Sequence 77583, A
C 44	18.6	47.7	660	7	US-11-217-529-1813	Sequence 1813, Ap
C 45	18.6	47.7	1011	7	US-11-217-529-173708	Sequence 173708, A

ALIGNMENTS

RESULT 1

US-10-953-349-17882
; Sequence 17882, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17882
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17882

Query Match 56.4%; Score 22; DB 6; Length 1556;
Best Local Similarity 73.7%; Pred. No. 5.7;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy	2	CCAAATTTTCATCCATTTGTTGTGATATAGTCTTCACA	39
Db	274	CAAAATGTCATCCAAATGATGTTGTTAGAAACATCACA	311

RESULT 2

US-11-217-529-1620
; Sequence 1620, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1620

; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1620

Query Match 53.3%; Score 20.8; DB 7; Length 1257;
Best Local Similarity 78.1%; Pred. No. 15;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TTTTGATCCATTGTTGTGATAGTCTTCAC 37
||||| ||||| ||||| ||||| |||||
Db 237 TTATGAAGCATTGTTGATATCATCTTCA 268
||||| ||||| ||||| ||||| |||||

RESULT 3
US-10-953-349-20828
; Sequence 20828, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20828
; LENGTH: 1262
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20828

Query Match 52.8%; Score 20.6; DB 6; Length 1262;
Best Local Similarity 74.3%; Pred. No. 18;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 CAATTTTGATCCATTGTTGTGATAGTCTTCA 37
||||| ||||| ||||| ||||| |||||
Db 1090 CAACTATGATCCCTTTGTTTAATATCATCTTCA 1124
||||| ||||| ||||| ||||| |||||

RESULT 4
US-11-217-529-3208/c
; Sequence 3208, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIOHKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3208
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3208

Query Match 52.3%; Score 20.4; DB 7; Length 678;
Best Local Similarity 71.1%; Pred. No. 19;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTGATAGTCTTCAG 38
||||| ||||| ||||| ||||| |||||

Db 595 CGCAATTTTCTCTGTTGCTGTGACGGTTGCTTGAG 558
||||| ||||| ||||| ||||| |||||

RESULT 5
US-10-953-349-3924
; Sequence 3924, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3924
; LENGTH: 1361
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3924

Query Match 51.8%; Score 20.2; DB 6; Length 1361;
Best Local Similarity 75.8%; Pred. No. 26;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 TTTTGATCCATTGTTGTGATAGTCTTTCAG 38
||||| ||||| ||||| ||||| |||||
Db 1205 TTTTGTCATTGCTTTGGATATGTTCTCTG 1237
||||| ||||| ||||| ||||| |||||

RESULT 6
US-11-217-529-77428/c
; Sequence 77428, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIOHKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77428
; LENGTH: 3075
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77428

Query Match 51.3%; Score 20; DB 7; Length 3075;
Best Local Similarity 72.2%; Pred. No. 35;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTGATAGTCTTC 36
||||| ||||| ||||| ||||| |||||
Db 2784 CCAATTTTATCATATTTCTGTTGTTATCTCC 2749
||||| ||||| ||||| ||||| |||||

RESULT 7
US-11-233-726-20/c
; Sequence 20, Application US/11233726
; Publication No. US20060090216A1
; GENERAL INFORMATION:
; APPLICANT: APUYA, Nestor
; APPLICANT: KWOK, Shing
; APPLICANT: ALEXANDROV, Nickolai

```

RESULT 9
US-11-217-529-75755/c
; Sequence 75755, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75755
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75755

Query Match 50.8%; Score 19.8; DB 7; Length 2772;
Best Local Similarity 77.4%; Pred. No. 41;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0

Qy 3 CAATTTTGATCCATTTTGTGTGATATAGTC 33
||| ||| ||| ||| ||| ||| ||| |||
Db 151 CAAACGTGAACGATTTGTGTGATTAAATC 121

RESULT 10

```

```

US-11-293-697-2392/C
; Sequence 2392, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2392
; LENGTH: 3230
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2392

Query Match          50.8%;   Score 19.8;   DB 7;   Length 3230;
Best Local Similarity 69.2%;   Pred. No. 42;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1  CCCAAATTTTGATCCCAFTTTGTTGTGATATAGTCTTCAGA 39
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      2212  CCCAACTTAGACTATTTCCTCTCTTATGGACCTGTGA 2174

RESULT 11
US-11-217-529-81556
; Sequence 81556, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHO

```

APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO

```

; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81556
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1767)..(1768)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-81556

Query Match      50.3%; Score 19.6; DB 7; Length 1794;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATTTGATCCATTGTTGTTGATATA 30
Db 929 ATTTGATCCATTGATGTTAATA 954
|||||
|||||

RESULT 12
US-10-953-349-6075
; Sequence 6075, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6075
; LENGTH: 1871
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6075

Query Match      50.3%; Score 19.6; DB 6; Length 1871;
Best Local Similarity 73.5%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 AATTTGATCCATTGTTGTTGATAGTCTTCA 37
Db 1760 AATTTGTTTATTGTTGTTTGAATAGTAGTTA 1793
|||||
|||||

RESULT 13
US-11-217-529-82386/c
; Sequence 82386, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80690
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80690/c

Query Match      49.7%; Score 19.4; DB 7; Length 1110;
Best Local Similarity 70.3%; Pred. No. 48;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 CCAATTTTCATCCATTGTTGTTGATATAGTCTTCAG 38
Db 377 CCAATTTTCATCCATCCGTTGTTGATATCTTTCAG 341
|||||
|||||

RESULT 14
US-11-217-529-1784/c
; Sequence 1784, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1784
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1784

Query Match      49.7%; Score 19.4; DB 7; Length 1110;
Best Local Similarity 70.3%; Pred. No. 48;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 CCAATTTTCATCCATTGTTGTTGATATAGTCTTCAG 38
Db 377 CCAATTTTCATCCATCCGTTGTTGATATCTTTCAG 341
|||||
|||||

RESULT 15
US-11-217-529-80690/c
; Sequence 80690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80690
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80690/c
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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82386
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82386

Query Match      49.7%; Score 19.4; DB 7; Length 810;
Best Local Similarity 70.3%; Pred. No. 45;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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```
QY 2 CCAATTTTCATCCATTGTTGTTGATATAGTCTTCAG 38
Db 377 CCAATTTTCATCCATTGTTGTTGATATCTTTCAG 341
|||||
|||||
```

```
RESULT 14
US-11-217-529-1784/c
; Sequence 1784, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1784
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1784
```

```
Query Match      49.7%; Score 19.4; DB 7; Length 1110;
Best Local Similarity 70.3%; Pred. No. 48;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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```
QY 2 CCAATTTTCATCCATTGTTGTTGATATAGTCTTCAG 38
Db 377 CCAATTTTCATCCATCCGTTGTTGATATCTTTCAG 341
|||||
|||||
```

```
RESULT 15
US-11-217-529-80690/c
; Sequence 80690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80690
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80690/c
```

```
Query Match      50.3%; Score 19.6; DB 6; Length 1871;
Best Local Similarity 73.5%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 AATTTGATCCATTGTTGTTGATAGTCTTCA 37
Db 1760 AATTTGTTTATTGTTGTTTGAATAGTAGTTA 1793
|||||
|||||

RESULT 13
US-11-217-529-82386/c
; Sequence 82386, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80690
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80690/c
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80690

Query Match 49.7%; Score 19.4; DB 7; Length 2130;
Best Local Similarity 70.3%; Pred. No. 54;
Matches 26; Conservative 0; Mismatches 11; Indels 0

Qy 2 CCAATTTGATCCATTGTGGTATAGTCTTCAG 38
 ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db , 1592 CGGAATTCATCAATTTGTCCTTGATGCTCTTAG 1556

Search completed: May 31, 2006, 21:22:05
Job time : 14.9259 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 87.1481 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-27

Perfect score: 39

Sequence: 1 tttttttttcttataatgattggtgattgttc 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*

Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	89	3	US-09-109-329-4
2	39	100.0	108	3	US-09-109-329-13
3	39	100.0	2007	2	US-08-743-637B-169
4	39	100.0	2007	3	US-08-526-840B-169
5	39	100.0	2028	3	US-09-134-001C-1710
6	29	74.4	59	3	US-09-109-329-3
7	25.2	64.6	3034	3	US-09-799-451-517
8	24.2	62.1	914	3	US-09-227-357-123
9	24.2	62.1	914	3	US-09-973-278-36
10	24.2	62.1	6254	3	US-08-956-171E-404
11	24.2	62.1	6254	3	US-08-781-986A-404
12	24.2	62.1	9262	3	US-09-566-921-74
13	24.2	62.1	107937	3	US-09-949-016-17192
14	24	61.5	36	3	US-09-109-329-14
15	24	61.5	36	3	US-09-109-329-15
16	23.6	60.5	601	3	US-09-949-016-188971
17	23.6	60.5	26664	3	US-09-564-805-28
18	23.6	60.5	26664	3	US-09-434-382-28
19	23.6	60.5	29558	3	US-09-949-016-15607
20	23.6	60.5	83349	3	US-09-949-016-17149
21	23.6	60.5	256287	3	US-09-949-016-14608
22	23	59.0	590	4	US-09-880-107-98
23	23	59.0	1210	3	US-09-023-655-594

24	23	59.0	2082	3	US-09-149-476-257	Sequence 257, App
25	23	59.0	60110	3	US-09-949-016-17338	Sequence 17338, A
26	23	59.0	60110	3	US-09-949-016-17339	Sequence 17339, A
27	23	59.0	61083	3	US-09-949-016-14144	Sequence 14144, A
28	23	59.0	61083	3	US-09-949-016-14145	Sequence 14145, A
29	22.6	57.9	601	3	US-09-949-016-161878	Sequence 161878, A
30	22.6	57.9	1848	3	US-09-323-998E-46	Sequence 46, Appl
31	22.6	57.9	2428	3	US-09-731-166-5	Sequence 5, Appl
32	22.6	57.9	36618	3	US-09-949-016-15723	Sequence 15723, A
33	22.6	57.9	49011	3	US-09-949-016-14221	Sequence 14221, A
34	22.6	57.9	65990	3	US-09-949-016-11830	Sequence 11830, A
35	22.6	57.9	144362	3	US-09-949-016-16066	Sequence 16066, A
36	22.6	57.9	153866	3	US-09-949-016-16919	Sequence 16919, A
37	22.6	57.9	238815	3	US-09-949-016-16274	Sequence 16274, A
38	22.2	56.9	13866	3	US-09-949-016-17252	Sequence 17252, A
39	22.2	56.9	44789	3	US-09-949-016-13909	Sequence 13909, A
40	22	56.4	601	3	US-09-949-016-85526	Sequence 85526, A
41	22	56.4	601	3	US-09-949-016-85527	Sequence 85527, A
42	22	56.4	601	3	US-09-949-016-178468	Sequence 178468, A
43	22	56.4	953	3	US-09-270-767-6678	Sequence 6678, Ap
44	22	56.4	953	3	US-09-270-767-21960	Sequence 21960, A
45	22	56.4	99830	3	US-09-949-016-16859	Sequence 16859, A

ALIGNMENTS

RESULT 1

US-09-109-329-4
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesis of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-4

Query Match 100.0%; Score 39; DB 3; Length 89;
Best Local Similarity 100.0%; Pred No. 0.00026;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTCTCTATTAATGATGCGATTGTC 39
|||||
DB 43 TTTTCTTTCTCTATTAATGATGCGATTGTC 81
|||||

RESULT 2

US-09-109-329-13/c
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-13

Query Match 100.0%; Score 39; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGCGATTGTATTGC 39
DB 49 TTTTCTTTTCTCTATTAAATGATGCGATTGTATTGC 11

RESULT 3
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994086
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5591
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match 100.0%; Score 39; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGCGATTGTATTGC 39
DB 49 TTTTCTTTTCTCTATTAAATGATGCGATTGTATTGC 11

RESULT 4
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5591
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 39; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGCGATTGTATTGC 39
DB 955 TTTTCTTTTCTCTATTAAATGATGCGATTGTATTGC 917

RESULT 5
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13


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; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      100.0%; Score 39; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATGATGCGGATGTTATGC 39
Db 976 TTTCTTTTCTCTATTATGATGCGGATGTTATGC 938

RESULT 6
US-09-109-329-3/c
; Sequence 3, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: STAPHYLOCOCCI
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-3

Query Match      74.4%; Score 29; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATGATGCGG 29
Db 29 TTTCTTTTCTCTATTATGATGCGG 1

RESULT 7
US-09-799-451-517
; Sequence 517, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aigong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
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; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 517
; LENGTH: 3034
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (729)..(917)
US-09-799-451-517

Query Match      64.6%; Score 25.2; DB 3; Length 3034;
Best Local Similarity 78.9%; Pred. No. 15;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATGATGCGGATGTTATGC 38
Db 2585 TATTTTGTATATATATGCTGTGTCGATGTTATGC 2622

RESULT 8
US-09-227-357-123/c
; Sequence 123, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
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; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (909)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-123

Query Match 62.1%; Score 24.2; DB 3; Length 914;
Best Local Similarity 78.4%; Pred. No. 29;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTTATATGATGCGATTGTATT 37
Db 872 TTTTCTTTTCTTATATGATGCGATTGTATT 836

RESULT 9
US-09-973-278-36/c
; Sequence 36, Application US/09973278
; Patent No. 6924354
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P2
; CURRENT APPLICATION NUMBER: US/09/973,278
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/239,899
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/051,926

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; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (909)
; OTHER INFORMATION: n equals a,t,g, or c

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US-09-973-278-36

Query Match 62.1%; Score 24.2; DB 3; Length 914;
Best Local Similarity 78.4%; Pred. No. 29;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTATGATGCGGATTCGATT 37
|||||
Db 872 TTTTCTTTTCTCTATTATGATGCGGATTCGATT 836

RESULT 10

US-08-956-171E-404/C

; Sequence 404, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-Oct-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 404:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6254 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 404:

US-08-956-171E-404

Query Match 62.1%; Score 24.2; DB 3; Length 6254;
Best Local Similarity 78.4%; Pred. No. 35;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTATGATGCGGATTCGATT 37
|||||
Db 2565 TTTTCTTTTCTCTATTATGATGCGGATTCGATT 2529

RESULT 11

US-08-781-986A-404/C

; Sequence 404, Application US/08781986A

; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-404

Query Match 62.1%; Score 24.2; DB 3; Length 6254;
Best Local Similarity 78.4%; Pred. No. 35;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTATGATGCGGATTCGATT 37
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Db 2565 TTTTCTTTTCTCTATTATGATGCGGATTCGATT 2529

RESULT 12

US-09-566-921-74

; Sequence 74, Application US/09566921

; Patent No. 6682888

; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.

; APPLICANT: Tingley, Debra W.

; APPLICANT: Edwards, Carla M.

; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE

; FILE REFERENCE: PA-0024 US

; CURRENT APPLICATION NUMBER: US/09/566,921

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: PERL Program

; SEQ ID NO 74

; LENGTH: 9262

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6682888 246655.92

; NAME/KEY: unsure

; LOCATION: 1941-1942, 1952-1953, 1956, 1958, 1963, 6600-6601

; OTHER INFORMATION: a, t, c, g, or other

US-09-566-921-74

Query Match		62.1%; Score 24.2; DB 3; Length 9262;
Best Local Similarity		78.4%; Pred. No. 36;
Matches		29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Db		
RESULT 13		
US-09-949-016-17192		
; Sequence 17192, Application US/09949016		
; Patent No. 6812339		
; GENERAL INFORMATION:		
; APPLICANT: VENTER, J. Craig et al.		
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED		
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF		
; FILE REFERENCE: CL001307		
; CURRENT APPLICATION NUMBER: US/09/949,016		
; CURRENT FILING DATE: 2000-04-14		
; PRIOR APPLICATION NUMBER: 60/241,755		
; PRIOR FILING DATE: 2000-10-20		
; PRIOR APPLICATION NUMBER: 60/237,768		
; PRIOR FILING DATE: 2000-10-03		
; PRIOR APPLICATION NUMBER: 60/231,498		
; PRIOR FILING DATE: 2000-09-08		
; NUMBER OF SEQ ID NOS: 207012		
; SOFTWARE: FastSeq for Windows Version 4.0		
; SEQ ID NO 17192		
; LENGTH: 107937		
; TYPE: DNA		
; ORGANISM: Human		
; FEATURE:		
; NAME/KEY: misc feature		
; LOCATION: (1)-(107937)		
; OTHER INFORMATION: n = A,T,C or G		
US-09-949-016-17192		
Query Match		62.1%; Score 24.2; DB 3; Length 107937;
Best Local Similarity		78.4%; Pred. No. 46;
Matches		29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy	1	TTTTCTTTTCTCTATTATGATGCGATTGTATT 37
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Db		
RESULT 14		
US-09-109-329-14/c		
; Sequence 14, Application US/09109329		
; Patent No. 6503709		
; GENERAL INFORMATION:		
; APPLICANT: Bekkaoui, Faouzi		
; APPLICANT: Cloney, Lynn P.		
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT		
; TITLE OF INVENTION: STAPHYLOCOCCI		
; FILE REFERENCE: 480094.424		
; CURRENT APPLICATION NUMBER: US/09/109,329		
; CURRENT FILING DATE: 1998-07-02		
; NUMBER OF SEQ ID NOS: 26		
; SOFTWARE: PatentIn Ver. 2.0		
; SEQ ID NO 14		
; LENGTH: 36		
; TYPE: DNA		
; ORGANISM: Artificial Sequence		
; FEATURE:		
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase		
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to		
; OTHER INFORMATION: mecA Gene from Staphylococcal Species		
US-09-109-329-14		
Query Match		61.5%; Score 24; DB 3; Length 36;

Best Local Similarity		100.0%; Pred. No. 25;
Matches		24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	TTTTCTTTTCTCTATTATTAATGTAT 24
	24	TTTTCTTTTCTCTATTATTAATGTAT 1
Db		
RESULT 15		
US-09-109-329-15/c		
; Sequence 15, Application US/09109329		
; Patent No. 6503709		
; GENERAL INFORMATION:		
; APPLICANT: Bekkaoui, Faouzi		
; APPLICANT: Cloney, Lynn P.		
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT		
; TITLE OF INVENTION: STAPHYLOCOCCI		
; FILE REFERENCE: 480094.424		
; CURRENT APPLICATION NUMBER: US/09/109,329		
; CURRENT FILING DATE: 1998-07-02		
; NUMBER OF SEQ ID NOS: 26		
; SOFTWARE: PatentIn Ver. 2.0		
; SEQ ID NO 15		
; LENGTH: 36		
; TYPE: DNA		
; ORGANISM: Artificial Sequence		
; FEATURE:		
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase		
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to		
; OTHER INFORMATION: mecA Gene from Staphylococcal Species		
US-09-109-329-15		
Query Match		61.5%; Score 24; DB 3; Length 36;
Best Local Similarity		100.0%; Pred. No. 25;
Matches		24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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	24	TTTTCTTTTCTCTATTATTAATGTAT 1
Db		
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Job time : 89.1481 secs		

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 1013.2 Seconds

(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-27

Perfect score: 39

Sequence: 1 tttttttttcttataatgattgctgattgttc 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pubmed Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	39	US-09-865-579A-27	Sequence 27, Appl
2	39	100.0	1957	US-10-479-674-82	Sequence 82, Appl
3	39	100.0	2007	US-09-452-599-169	Sequence 169, Appl
4	39	100.0	2007	US-10-121-120-169	Sequence 169, Appl
5	39	100.0	2007	US-10-479-674-78	Sequence 78, Appl
6	39	100.0	2007	US-10-479-674-90	Sequence 90, Appl
7	39	100.0	2007	US-10-479-674-91	Sequence 91, Appl
8	39	100.0	2007	US-10-121-120-169	Sequence 169, Appl
9	39	100.0	2028	US-10-724-972A-3141	Sequence 3141, Appl
10	25.2	64.6	3034	US-10-302-172-517	Sequence 517, Appl
11	24.6	63.1	644	US-09-925-065A-827806	Sequence 827806, Appl
12	24.6	63.1	644	US-09-925-065A-827807	Sequence 827807, Appl
13	24.6	63.1	644	US-09-925-065A-827806	Sequence 827806, Appl
14	24.6	63.1	644	US-09-925-065A-827807	Sequence 827807, Appl
15	24.2	62.1	343	US-10-674-124A-21698	Sequence 21698, A
16	24.2	62.1	685	US-10-027-632-109982	Sequence 109982, A
17	24.2	62.1	685	US-10-027-632-109982	Sequence 109982, A

C 18	24.2	62.1	699	3	US-09-815-242-4505	Sequence 4505, Ap
C 19	24.2	62.1	699	3	US-09-815-242-8471	Sequence 8471, Ap
C 20	24.2	62.1	699	8	US-10-282-122A-7879	Sequence 7879, Ap
C 21	24.2	62.1	821	6	US-10-106-698-1828	Sequence 1828, Ap
C 22	24.2	62.1	914	3	US-09-983-802-123	Sequence 123, App
C 23	24.2	62.1	914	3	US-09-984-490-123	Sequence 123, App
C 24	24.2	62.1	914	3	US-09-973-278-36	Sequence 36, Appl
C 25	24.2	62.1	986	12	US-10-301-480-59809	Sequence 59809, A
C 26	24.2	62.1	986	12	US-10-301-480-1203218	Sequence 1203218, A
C 27	24.2	62.1	987	12	US-10-301-480-59808	Sequence 59808, A
C 28	24.2	62.1	987	12	US-10-301-480-1203217	Sequence 1203217, A
C 29	24.2	62.1	1044	7	US-10-174-209-31	Sequence 31, Appl
C 30	24.2	62.1	1044	10	US-10-972-587-31	Sequence 31, Appl
C 31	24.2	62.1	1244	12	US-10-986-405-121	Sequence 121, Appl
C 32	24.2	62.1	6254	2	US-08-781-986A-404	Sequence 404, App
C 33	24.2	62.1	6254	8	US-10-329-624-404	Sequence 74, App
C 34	24.2	62.1	9262	10	US-10-765-700-74	Sequence 95, Appl
C 35	24.2	62.1	9277	6	US-10-084-817-95	Sequence 55048, A
C 36	23.8	61.0	245	8	US-10-424-599-55048	Sequence 420484, A
C 37	23.8	61.0	569	4	US-09-925-065A-420484	Sequence 420484, A
C 38	23.8	61.0	569	5	US-09-925-065A-420484	Sequence 420484, A
C 39	23.8	61.0	569	12	US-10-301-480-485470	Sequence 1098879, A
C 40	23.8	61.0	569	12	US-10-301-480-1098879	Sequence 9980, App
C 41	23.6	60.5	201	15	US-11-124-368A-9980	Sequence 756577, A
C 42	23.6	60.5	465	4	US-09-925-065A-756577	Sequence 756577, A
C 43	23.6	60.5	465	5	US-09-925-065A-756577	Sequence 14453, A
C 44	23.6	60.5	742	4	US-09-925-065A-14453	Sequence 14453, A
C 45	23.6	60.5	742	5	US-09-925-065A-14453	Sequence 14453, A

ALIGNMENTS

RESULT 1

US-09-865-579A-27
; Sequence 27, Application US/09865579A
; Patent No. US2002009492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Saio, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-27

Query Match 100.0%; Score 39; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTTCTTATGATGATGCGATTGTTC 39
Db 1 TTTTCTTTTCTTCTTATGATGATGCGATTGTTC 39

RESULT 2

US-10-479-674-82/C
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1

```

; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANCE
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 39; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
DB 905 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 867

RESULT 3
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US2002005101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 39; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
DB 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 4
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers

```

```

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 39; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
DB 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 5
US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIS
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match      100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
DB 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 6
US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIS
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match 100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTGCGGATTGTATTGC 39
|||||
Db 955 TTTTCTTTTCTCTATTAAATGATGTGCGGATTGTATTGC 917

RESULT 7

US-10-479-674-91/c
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match 100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTGCGGATTGTATTGC 39
|||||
Db 955 TTTTCTTTTCTCTATTAAATGATGTGCGGATTGTATTGC 917

RESULT 8

US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-10-121-120-169

Query Match 100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTGCGGATTGTATTGC 39
|||||
Db 955 TTTTCTTTTCTCTATTAAATGATGTGCGGATTGTATTGC 917

RESULT 9

US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match 100.0%; Score 39; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTGCGGATTGTATTGC 39
|||||
Db 976 TTTTCTTTTCTCTATTAAATGATGTGCGGATTGTATTGC 938

RESULT 10

US-10-302-172-517
; Sequence 517, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. US20040053250A1 Arginine-rich Protein-like Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803.1CNCp
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 517
; LENGTH: 3034
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827807
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-827807

Query Match 63.1%; Score 24.6; DB 5; Length 644;
Best Local Similarity 76.9%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0; /
QY 1 TTTTCTTTTCTCTATTATGATGCGGATGCTATTGC 39
DB 187 TCTTCTCTTTTACTCTTAATGATGCGCGGATGCTTTTC 149

RESULT 15

US-10-674-124A-21698/c
; Sequence 21698, Application US/10674124A
; Publication No. US20040197797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 21698
; LENGTH: 343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: D15S657
; FEATURE:
; OTHER INFORMATION: Located on chromosome 15
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 93129500
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 125770
US-10-674-124A-21698

Query Match 62.1%; Score 24.2; DB 9; Length 343;
Best Local Similarity 78.4%; Pred. No. 4.7e+02;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATGATGCGGATGCTATT 37
DB 91 TATTCCTTTTCTATATATATATGCGGAAGTGTT 55

Search completed: May 31, 2006, 23:02:26
Job time : 1014.2 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 14.9259 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-27

Perfect score: 39

Sequence: 1 ttttttttcttataatgattggtattgttc 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22.6	57.9	1848	6	US-10-524-648-25 Sequence 25, Appl
2	22.6	57.9	2506	6	US-10-524-648-25 Sequence 34173, A
3	22.2	56.9	985	6	US-10-524-648-25 Sequence 6094, Ap
C 4	22	56.4	3354	7	US-11-217-529-1206 Sequence 1206, Ap
C 5	21.6	55.4	138941	6	US-10-489-730-10 GENERAL INFORMAT
6	21	53.8	213	7	US-11-217-529-77446 Sequence 77446, A
7	21	53.8	653	6	US-10-524-648-25 Sequence 14981, A
C 8	21	53.8	1478	1	US-09-949-925-56 Sequence 56, Appl
C 9	21	53.8	1769	6	US-10-524-648-25 Sequence 22788, A
C 10	21	53.8	1789	6	US-10-524-648-25 Sequence 13689, A
11	20.6	52.8	1795	6	US-10-524-648-25 Sequence 3907, Ap
12	20.4	52.3	728	6	US-10-524-648-25 Sequence 24115, A
13	20.4	52.3	1451	6	US-10-524-648-25 Sequence 11528, A
14	20.4	52.3	2150	6	US-10-524-648-25 Sequence 19450, A
C 15	20.4	52.3	2835	7	US-11-217-529-5468 Sequence 5468, Ap
C 16	20	51.3	753	6	US-10-524-648-25 Sequence 9366, Ap
17	20	51.3	882	6	US-10-524-648-25 Sequence 26378, A
18	20	51.3	2575	7	US-11-293-697-894 Sequence 894, Appl
C 19	20	51.3	42999	7	US-11-284-877-17 Sequence 17, Appl
C 20	19.8	50.8	1116	7	US-11-217-529-80347 Sequence 80347, A
21	19.8	50.8	1325	6	US-10-524-648-25 Sequence 3793, Ap
22	19.8	50.8	2187	7	US-11-293-697-1171 Sequence 1171, Ap
C 23	19.8	50.8	2754	7	US-11-217-529-79792 Sequence 79792, A
C 24	19.8	50.8	3524	7	US-11-293-697-454 Sequence 454, Appl
C 25	19.6	50.3	759	7	US-11-217-529-76103 Sequence 76103, A

RESULT 1

US-10-524-648-25/c
; Sequence 25, Application US/10524648
; Publication No. US20060107352A1

GENERAL INFORMATION:

APPLICANT: Schopfer, Christel

APPLICANT: Sauer, Matt

APPLICANT: Klebsattel, Martin

APPLICANT: Flachmann, Ralf

TITLE OF INVENTION: Transgenic expression cassettes for expressing nucleic acids in

FILE REFERENCE: 13173-00002-US

CURRENT APPLICATION NUMBER: US/10/524,648

CURRENT FILING DATE: 2005-02-17

PRIOR APPLICATION NUMBER: PCT/EP 03/008394

PRIOR FILING DATE: 2003-07-30

PRIOR APPLICATION NUMBER: DE 102 38 979.9

PRIOR FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: DE 102 47 599.7

PRIOR FILING DATE: 2002-02-11

NUMBER OF SEQ ID NOS: 83

SOFTWARE: PatentIn version 3.3

SEQ ID NO 25

LENGTH: 1848

TYPE: DNA

ORGANISM: Adonis palaeatina

FEATURE:

NAME/KEY: CDS

LOCATION: (116)..(1702)

OTHER INFORMATION: coding for epsilon cyclase

US-10-524-648-25

Query Match 57.9%; Score 22.6; DB 6; Length 1848;

Best Local Similarity 75.7%; Pred. No. 15;

Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TTTTCTTTCTCTATTATGATGCGATTGTATT 37

||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1838 TTTTCTTTCTCTATTATGATGCGATTGTATT 1802

RESULT 2

US-10-953-349-34173

; Sequence 34173, Application US/109533349

; Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

ORGANISM: SACCO
IIS-11-217-529-1206

QY 5 CTTTTCCTCTATTAAATGTATGTGCGATTG 33

US-10-953-349-3907
; Sequence 3907, Application US/10953349
; Publication No. US20060107345A1

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; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3907
; LENGTH: 1795
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3907

Query Match          52.8%; Score 20.6; DB 6; Length 1795;
Best Local Similarity 74.3%; Pred. No. 66;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TTTCTTTTCTCTAATGATGATGCGGATTGTAT 36
    ||||| ||||| ||||| ||||| ||||| |||||
Db 1602 TATCTATCTATATATATATATATCCGATTGTAT 1636

RESULT 12
US-10-953-349-24115
; Sequence 24115, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24115
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-24115

Query Match          52.3%; Score 20.4; DB 6; Length 728;
Best Local Similarity 71.1%; Pred. No. 68;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTAATGATGATGCGGATTGTATG 38
    ||||| ||||| ||||| ||||| ||||| |||||
Db 687 TTCCCTTTTGTATTAATGATGATGCGGATTGTATG 724

RESULT 13
US-10-953-349-11528
; Sequence 11528, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11528
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11528

Query Match          52.3%; Score 20.4; DB 6; Length 1451;
Best Local Similarity 71.1%; Pred. No. 74;

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Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTAATGATGATGCGGATTGTATG 38
    ||||| ||||| ||||| ||||| ||||| |||||
Db 1333 TTTTCTTTTGTGTGTGTGTGTGTGTGTGTGTG 1370

RESULT 14
US-10-953-349-19450
; Sequence 19450, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19450
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-19450

Query Match          52.3%; Score 20.4; DB 6; Length 2150;
Best Local Similarity 71.1%; Pred. No. 78;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTAATGATGATGCGGATTGTATG 38
    ||||| ||||| ||||| ||||| ||||| |||||
Db 113 TTTTCTTTTGTGTGTGTGTGTGTGTGTGTGTG 150

RESULT 15
US-11-217-529-5468/c
; Sequence 5468, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5468
; LENGTH: 2835
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5468

Query Match          52.3%; Score 20.4; DB 7; Length 2835;
Best Local Similarity 71.1%; Pred. No. 80;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 TTTCTTTTCTCTAATGATGATGCGGATTGTATGC 39
    ||||| ||||| ||||| ||||| ||||| |||||
Db 244 TCTCTTTTCTATACTAATATCAGGGCTTTTGATAGC 207

Search completed: May 31, 2006, 21:22:06
Job time : 15.9259 secs

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